

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 31.2821 Seconds  
(without alignments)  
170.386 Million cell updates/sec

Title: US-09-780-438c-1

Perfect score: 211

Sequence: 1 SDYCVCFVKEVTKLIDNNKTEKILDAFDKMGSKLP 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	80	AAW70784	Saposin-C. Homo s
2	211	100.0	80	AAW85653	Human saposin C.
3	211	100.0	80	AAU05697	Human Saponin C, S
4	211	100.0	523	AAAB31916	Amino acid sequenc
5	211	100.0	524	AAW70783	Prosaposin. Homo
6	211	100.0	524	AAW85652	Human prosaposin N
7	211	100.0	524	AAW58716	Human prosaposin.
8	211	100.0	527	AAAB31915	Amino acid sequenc
9	211	100.0	592	AAU05698	Human glucocerebro
10	127	60.2	25	AAW67289	Human saposin C.

11	111	52.6	22	16	AAW70773	Saposin-C neurotro
12	111	52.6	22	18	AAW30013	Prosaposin-derived
13	111	52.6	22	19	AAW66127	Prosaposin recepto
14	111	52.6	22	20	AAW85656	Prosaposin recepto
15	111	52.6	22	22	AAW67305	Peptide #5. Homo
16	106	50.2	22	18	AAW30028	Mutant human prosa
17	106	50.2	22	18	AAW30028	Prosaposin derivat
18	103	48.8	21	21	AAW66134	Human saposin C 22
19	99	46.9	25	22	AAW82281	Bovine saposin C
20	96	45.5	22	22	AAW67293	Bovine prosaposin-
21	96	45.5	22	18	AAW30018	Prosaposin recepto
22	96	45.5	22	20	AAW85661	Prosaposin recepto
23	83	39.3	18	16	AAW70785	Saposin-C derived
24	83	39.3	18	18	AAW30031	Saposin C 12 to 29
25	83	39.3	18	19	AAW66146	Prosaposin recepto
26	83	39.3	18	20	AAW85655	Prosaposin recepto
27	83	39.3	18	21	AAW82282	Human saposin C 18
28	80	37.9	25	22	AAW67292	Guinea pig saposin
29	78	37.0	554	23	ABW57102	Mouse ischaemic co
30	75	35.5	15	19	AAW83412	Human saposin C de
31	75	35.5	15	19	AAW99848	Human saposin C fr
32	75	35.5	15	21	AAW83914	Human saposin C pe
33	75	35.5	22	18	AAW30017	Guinea pig prosapo
34	75	35.5	22	19	AAW66132	Prosaposin recepto
35	75	35.5	22	20	AAW85660	Prosaposin recepto
36	73	34.6	514	23	ABW07483	Theobroma cacao as
37	73	34.6	514	23	ABW07487	Drosophila melanog
38	73	34.6	953	22	ABW58389	Arabidopsis thalia
39	70	33.2	149	21	AAW35693	Arabidopsis thalia
40	70	33.2	205	21	AAW35692	Arabidopsis thalia
41	70	33.2	298	21	AAW17819	Arabidopsis thalia
42	70	33.2	506	21	AAW17818	Arabidopsis thalia
43	70	33.2	522	21	AAW17817	Arabidopsis thalia
44	67	31.8	80	22	AAW86360	Human esAP-C prote
45	67	31.8	345	22	AAW01850	Human gene 1 encod

ALIGNMENTS

RESULT 1

AAW70784  
ID AAR70784 standard; Protein; 80 AA.

XX AC AAR70784;

XX DT 30-AUG-1995 (first entry)

XX DE Saposin-C.

XX OS Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
XX PN neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
XX FN adrenal leukodystrophy.

XX OS Homo sapiens.

XX PN WO9503821-A.

XX FD 09-FEB-1995.

XX PF 28-JUL-1994; 94WO-US08453.

XX PR 30-JUL-1993; 93US-0100247.

XX PR 21-APR-1994; 94US-0232513.

(OBRI/) OBRIEN-J-S.

XX Kishimoto Y, Obrien JS;

XX WPI; 1995-082029/11.

XX Stimulating neural cell out-growth and myelination - with  
PT pro:saposin, saposin C or new neurotrophic peptide(s) from

PT cytokine(s), for treating nervous system diseases

XX Disclosure; Page 32; 50pp; English.

XX The peptide given in AAR70773, corresponding to amino acids 8-29 of  
 CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
 CC A consensus sequence was determined by comparing the peptide with  
 CC hematopoietic and neurotrophic cytokines, and neurotrophic peptides  
 CC (AAR70774-82) were identified in the AB loop of human ciliary  
 CC neurotrophic factor, interleukins-6, -2, -3 and -gamma.  
 CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
 CC human interleukin-1-beta and oncostatin-M. Prosapoin (AAR70783)  
 CC and saposin-C also promoted nerve cell myelination ex vivo.

XX Sequence 80 AA;

Query Match 100.0%; Score 211; DB 16; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKVETKLIDNNKTEKEILDADFDMCKSLP 40

Db 1 SDVYCEVCEFLVKVETKLIDNNKTEKEILDADFDMCKSLP 40

RESULT 2

AAW85653

ID AAW85653 standard; Peptide; 80 AA.

XX AAW85653;

DT 19-JUL-1999 (first entry)

DE Human saposin C.

XX Prosapoin; saposin; prosaptides; prosapoin receptor agonists;  
 KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
 KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
 KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
 KW inflammation; rheumatoid arthritis; Crohn's disease;  
 KW irritable bowel syndrome; asthma; cardiac infarction;  
 KW congestive heart failure; multiple sclerosis;  
 KW acute disseminated inflammatory leukoencephalitis;  
 KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
 KW Parkinson's disease; amyotrophic lateral sclerosis;  
 KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
 KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
 KW inflammatory neurodegenerative disease; toxin-induced liver disease.

XX Homo sapiens.

XX WO9912559-A1.

PN 18-MAR-1999.

XX 09-SEP-1998; 98WO-US19216.

XX 04-JUN-1998; 98US-0088129.

PR 09-SEP-1997; 97US-0058352.

XX (REGC ) UNIV CALIFORNIA.

XX O'brien JS;

DR WPI; 1999-229139/19.

XX Use of prosapoin receptor agonist

XX Claim 7; Figure 2; 90pp; English.

XX Prosapoin is a 70kDa glycoprotein which is proteolytically processed  
 CC to generate saposins A, B, C and D, all of which are similar to each  
 CC other and have a similar placement of six cysteines, a glycosylation

CC site and conserved proline residues. Prosapoin, saposin C and  
 CC prosapoin derived peptides (prosaptides), have therapeutic  
 CC applications in promoting recovery after toxic, traumatic, myocardial  
 CC ischaemic, degenerative and inherited lesions to the peripheral and  
 CC central nervous system. Prosapoin receptor agonists (PRAS)  
 CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
 CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
 CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
 CC members which inhibit caspases, thereby inhibiting apoptosis. An  
 CC additional mechanism whereby PRAS inhibit apoptosis is by blocking  
 CC activation of JNK, a proapoptotic signaling component. Within  
 CC several minutes after binding to the receptor, PRAS block JNK  
 CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
 CC activation of JNK by TNF alpha is another well known mechanism for  
 CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
 CC apoptosis. The method can be used for inhibiting apoptosis which is  
 CC caspase-mediated or induced by a proinflammatory cytokine, for  
 CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
 CC apoptosis associated with a disorder such as e.g. rheumatoid  
 CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
 CC infarction, congestive heart failure, multiple sclerosis, acute  
 CC disseminated inflammatory leukoencephalitis, progressive multifocal  
 CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
 CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
 CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
 CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
 CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
 CC liver disease. Saposin C acts as a prosapoin receptor agonist.

XX Sequence 80 AA;

Query Match 100.0%; Score 211; DB 20; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKVETKLIDNNKTEKEILDADFDMCKSLP 40

Db 1 SDVYCEVCEFLVKVETKLIDNNKTEKEILDADFDMCKSLP 40

RESULT 3

AAU05697

ID AAU05697 standard; Protein; 80 AA.

XX AAU05697;

XX 24-OCT-2001 (first entry)

DE Human Saponin C, SapC.

XX Human; glucocerebrosidase; GCB; lysosomal storage disease;

KW Gaucher's disease; Fabry's disease; Farber's disease;

KW G.m.1 gangliosidosis; Tay-Sachs's disease; Niemann-pick disease;

KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;

KW Schelte syndrome; Saponin C; SapC.

XX Homo sapiens.

XX WO200149830-A2.

XX 12-JUL-2001.

XX 29-DEC-2000; 2000WO-DK00743.

XX 30-DEC-1999; 99DK-0001891.

PR 02-JUN-2000; 2000DK-0000865.

PR 02-JUN-2000; 2000DK-0000866.

PR 30-JUN-2000; 2000DK-0001027.

XX (MAXY-) MAXYGEN APS.

XX Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;

DR WPI; 2001-465259/50.  
XX Improved lysosomal enzymes and lysosomal enzyme activators useful for  
PT treating Gaucher's disease  
XX Example 5; Page 96; 97pp; English.  
XX The sequence represents human Saponin C (SapC), an essential  
CC co-factor for the lysosomal enzyme glucocerebrosidase, a lysosomal  
CC GCB. GCB is the enzyme involved in Gaucher's disease, a lysosomal  
CC storage disease. The invention relates to introducing new glycosylation  
CC sites into lysosomal enzymes/activators like GCB to improve their  
CC bioactivity. The novel polypeptides are used for the prevention and  
CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,  
CC G.M.I. gangliosidosis, Tay-Sach's disease, Niemann-Pick disease, Shindler  
CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie  
CC syndromes.  
XX  
SQ Sequence 80 AA;  
Query Match 100.0%; Score 211; DB 22; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9.9e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40  
RESULT 4  
AAB31916  
ID AAB31916 standard; Protein: 523 AA.  
XX AC AAB31916;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Amino acid sequence of a human protein.  
XX  
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;  
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;  
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200105422-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 17-JUL-2000; 2000WO-FR02057.  
XX  
PR 15-JUL-1999; 99FR-0009372.  
XX  
PA (INMR) BIOMERIEUX STELHYS.  
XX  
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;  
XX  
DR WPI; 2001-159475/16.  
XX  
XX Detecting, preventing and treating degenerative, neurological and  
PT autoimmune diseases, particularly multiple sclerosis, using specified  
PT polypeptides or related nucleic acid or ligand  
XX  
PS Claim 1; Page 174-175; 209pp; French.  
XX  
CC The present sequence represents a human protein, which is used in the  
CC method of the invention. The specification describes a method which uses  
CC at least one polypeptide or polynucleotide sequence belonging to the  
CC perlecan, precursor of the retinol-binding plasma protein, precursor of  
CC the ganglioside GM2 activator, calgranulin B or saposin B protein  
CC families. The method is used for detecting, preventing or treating a

CC degenerative, neurological and/or auto-immune disease. The  
CC polynucleotides and polypeptides are used for diagnosis, prognosis,  
CC prevention and treatment of multiple sclerosis (in its various forms  
CC and phases). They may also be useful in cases of e.g. Alzheimer's and  
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid  
CC polyarthritis and lupus erythematosus, including use as vaccines and  
CC in gene therapy (expression of sense or antisense sequences). They can  
CC also be used to assess efficacy of potential therapeutic agents,  
CC particularly compounds that reduce or inhibit toxicity towards glial  
CC cells.  
XX  
SQ Sequence 523 AA;  
Query Match 100.0%; Score 211; DB 22; Length 523;  
Best Local Similarity 100.0%; Pred. No. 8.7e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40  
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 349  
RESULT 5  
AAR70783  
ID AAR70783 standard; Protein: 524 AA.  
XX AC AAR70783;  
XX  
XX 30-AUG-1995 (first entry)  
DE Prosaposin.  
XX  
KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW adrenal leukodystrophy; prosaposin.  
XX  
OS Homo sapiens.  
XX  
PN WO9503821-A.  
XX  
PD 09-FEB-1995.  
XX  
PF 28-JUL-1994; 94WO-US08453.  
XX  
PR 30-JUL-1993; 93US-0100247.  
PR 21-APR-1994; 94US-022513.  
XX  
PA (OBRI) OBRIEN J S.  
XX  
PI Kishimoto Y, Obrien JS;  
XX  
DR WPI; 1995-082029/11.  
DR N-PSDB; AAQ85355.  
XX  
XX Stimulating neural cell out-growth and myelination - with  
PT pro:saposin, saposin C or new neurotrophic peptide(s) from  
PT cytokine(s), for treating nervous system diseases  
XX  
PS Disclosure; Page 30-32; 50pp; English.  
XX  
CC The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neurotrophic cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosaposin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.  
XX  
SQ Sequence 524 AA;  
Query Match 100.0%; Score 211; DB 16; Length 524;

Best Local Similarity 100.0%; Pred. No. 8.8e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
|||||  
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 350

RESULT 6  
AAW85652  
ID AAW85652 standard; Protein: 524 AA.  
XX  
AC AAW85652;  
XX  
DT 19-JUL-1999 (first entry)  
XX  
DE Human prosaposin N-terminal peptide.  
XX  
KW Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
XX WO912559-A1.  
PN  
XX  
PD 18-MAR-1999.  
XX  
PF 09-SEP-1998; 98WO-US19216.  
PR  
PR 04-JUN-1998; 98US-0088129.  
PR 09-SEP-1997; 97US-0058352.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PI  
PI O'brien JS;  
XX  
DR WPI: 1999-229139/19.  
DR N-PSDB; AAX08488.  
XX  
PT Use of prosaposin receptor agonist  
XX  
PS Claim 7; Figure 2; 90pp; English.  
XX  
CC Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
CC to generate saposins A, B, C and D, all of which are similar to each  
CC other and have a similar placement of six cysteines, a glycosylation  
CC site and conserved proline residues. Prosaposin, saposin C and  
CC prosaposin derived peptides (prosaptides), have therapeutic  
CC applications in promoting recovery after toxic, traumatic, myocardial  
CC ischaemic, degenerative and inherited lesions to the peripheral and  
CC central nervous system. Prosaposin receptor agonists (PRAs)  
CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
CC members which inhibit caspases, thereby inhibiting apoptosis. An  
CC additional mechanism whereby PRAs inhibit apoptosis is by blocking  
CC activation of JNK, a proapoptotic signaling component. Within  
CC several minutes after binding to the receptor, PRAs block JNK  
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
CC activation of JNK by TNF alpha is another well known mechanism for  
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
CC apoptosis. The method can be used for inhibiting apoptosis which is

CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC as a prosaposin receptor agonist.  
XX  
SQ Sequence 524 AA;  
Query Match 100.0%; Score 211; DB 20; Length 524;  
Best Local Similarity 100.0%; Pred. No. 8.8e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
|||||  
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 350

RESULT 7  
AAW58716  
ID AAY58716 standard; Protein: 524 AA.  
XX  
AC AAY58716;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human prosaposin.  
XX  
KW Prosaposin; saponin B; antiangiogenic; angiogenesis inhibitor;  
KW antitumour; antiproliferative; antimigratory; Kaposi's sarcoma;  
KW tumour; human; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FH Protein 195..275  
FT /note= "mature saposin B"  
FT Peptide 195..205  
FT /note= "specifically claimed antiangiogenic peptide  
FT of Claim 23"  
FT Peptide 196..200  
FT /note= "specifically claimed antiangiogenic peptide  
FT of Claim 4"  
XX  
PN WO200002902-A1.  
XX  
PD 20-JAN-2000.  
XX  
PF 12-JUL-1999; 99WO-US15772.  
XX  
PR 13-JUL-1998; 98US-0092647.  
XX  
PA (GILL/) GILL P S.  
XX  
PI Gill PS;  
XX  
DR WPI: 2000-171128/15.  
XX  
PT Saposin B derived peptides, useful as inhibitors of angiogenesis and  
PT tumor growth -  
XX  
PS Disclosure; Page 18; 78pp; English.  
XX  
CC The present sequence is that of human prosaposin, a precursor of  
CC saposin B. The invention is based on the discovery that saposin B,  
CC previously known to be involved in the hydrolysis of sphingolipids,

CC has potent antiangiogenic and antitumour activity, and also has  
 CC antiproliferative and antimigratory activity against endothelial  
 CC cells. This activity is conserved in cryptic polypeptides as small  
 CC as 5 amino acids (see AAY58684-715), which can be synthetically  
 CC prepared and used in vitro or in vivo for the treatment of  
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma  
 CC (claimed). The polypeptides can also be used in conjunction with  
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for  
 CC treatment of cancer, angiofibroma, neovascular glaucoma,  
 CC arteriovenous malformation, nonunion fracture, arthritis and other  
 CC connective tissue disorders, Osler-Weber syndrome, atherosclerotic  
 CC plaque, psoriasis, corneal graft neovascularization, pyogenic  
 CC granuloma, retrolental fibroplasia, diabetic retinopathy,  
 CC scleroderma, haemangioma, trachoma, vascular adhesions and  
 CC hypertrophic scars.

XX Sequence 524 AA;

Query Match 100.0%; Score 211; DB 21; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-19;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
 DB 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 350

RESULT 8

AAB31915  
 ID AAB31915 standard; Protein; 527 AA.

XX AAB31915;

DT 15-MAY-2001 (first entry)

DE Amino acid sequence of a human protein.

XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;  
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;  
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;  
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX Homo sapiens.

XX WO200105422-A2.

XX 25-JAN-2001.

XX 17-JUL-2000; 2000WO-FR02057.

XX 15-JUL-1999; 99FR-0009372.

XX (INMR ) BIOMERIEUX STELHYS.

XX Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX WPI; 2001-159475/16.

XX Detecting, preventing and treating degenerative, neurological and  
 PT autoimmune diseases, particularly multiple sclerosis, using specified  
 PT polypeptides or related nucleic acid or ligand

PS Claim 1; Page 172-173; 209pp; French.

XX The present sequence represents a human protein, which is used in the  
 CC method of the invention. The specification describes a method which uses  
 CC at least one polypeptide or polynucleotide sequence belonging to the  
 CC perlecan, precursor of the retinol-binding plasma protein, precursor of  
 CC the ganglioside GM2 activator, calgranulin B or saposin B protein  
 CC families. The method is used for detecting, preventing or treating a  
 CC degenerative, neurological and/or auto-immune disease. The  
 CC polynucleotides and polypeptides are used for diagnosis, prognosis,

CC prevention and treatment of multiple sclerosis (in its various forms  
 CC and phases). They may also be useful in cases of e.g. Alzheimer's and  
 CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid  
 CC polyarthritis and lupus erythematosus, including use as vaccines and  
 CC in gene therapy (expression of sense or antisense sequences). They can  
 CC also be used to assess efficacy of potential therapeutic agents,  
 CC particularly compounds that reduce or inhibit toxicity towards glial  
 CC cells.

XX Sequence 527 AA;

Query Match 100.0%; Score 211; DB 22; Length 527;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-19;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
 DB 314 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 353

RESULT 9

AAU05698  
 ID AAU05698 standard; Protein; 592 AA.

XX AAU05698;

XX 24-OCT-2001 (first entry)

XX Human glucocerebrosidase, GCB-Saponin C, SapC, fusion protein.

XX Human; glucocerebrosidase; GCB; lysosomal storage disease;

KW Gaucher's disease; Fabry's disease; Farber's disease;

KW G.M.1 gangliosidosis; Tay-Sachs's disease; Niemann-Pick disease;

KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;

KW Scheie syndrome; fusion protein; Saponin C; SapC.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

PH Protein 1..80

FT Peptide 81..95 /label= SapC

FT Peptide 96..592 /label= Linker\_peptide

FT Protein 114 /label= GCB

FT Modified-site 154 /note= "N-glycosylated"

FT Modified-site 241 /note= "N-glycosylated"

FT Modified-site 365 /note= "N-glycosylated"

FT Modified-site 365 /note= "N-glycosylated"

XX WO200149830-A2.

XX 12-JUL-2001.

XX 29-DEC-2000; 2000WO-DK00743.

XX 30-DEC-1999; 99DK-0001891.

PR 02-JUN-2000; 2000DK-0000865.

PR 02-JUN-2000; 2000DK-0000866.

PR 30-JUN-2000; 2000DK-0001027.

XX (MAXY-) MAXYGEN APS.

XX Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;

XX WPI; 2001-465259/50.

XX Improved lysosomal enzymes and lysosomal enzyme activators useful for

PT treating Gaucher's disease -

PS Example 5; Page 96-97; 97pp; English.

XX The sequence is a fusion protein of human lysosomal enzyme  
CC glucocerebrosidase, GCB and its co-factor, Saponin C, SapC.  
CC GCB is the enzyme involved in Gaucher's disease, a lysosomal  
CC storage disease. The invention relates to introducing new glycosylation  
CC sites into lysosomal enzymes/activators like GCB to improve their  
CC bioactivity. The novel polypeptides are used for the prevention and  
CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,  
CC G\_m\_1 gangliosidosis, Tay-Sach's disease, Niemann-Pick disease, Shindler  
CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie  
CC syndromes.

XX Sequence 592 AA;

Query Match 100.0%; Score 211; DB 22; Length 592;

Best Local Similarity 100.0%; Pred. No. 1e-18;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

RESULT 10

AAB67289

ID AAB67289 standard; Peptide; 25 AA.

XX AAB67289;

XX 20-APR-2001 (first entry)

XX Human saposin C.

XX Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.

XX Homo sapiens.

XX EP1072609-A2.

XX 31-JAN-2001.

XX 30-JUN-2000; 2000EP-0305504.

XX 30-JUN-1999; 99JP-0185155.

XX (SAKA/) SAKANAKA M.

XX (TANA/) TANAKA J.

XX (SATO/) SATO K.

XX Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;

XX WPI; 2001-204263/21.

XX Use of prosaposin-related peptides or derivatives as cytoprotective  
PT agents, for suppressing apoptosis or apoptosis-like cell death -

PS Disclosure; Page 12; 41pp; English.

XX The present invention relates to use of a prosaposin-related peptide  
CC or derivative, in the production of a medicament for use in  
CC preventing or delaying cell death, or in promoting the expression  
CC of cell death supporting gene product Bcl-XL. The invention is  
CC useful for preventing the death of cells e.g. brain cells,  
CC neurons and cardiac muscle cells, in vitro or ex vivo.

XX Sequence 25 AA;

Query Match 60.2%; Score 127; DB 22; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEILDADF 32

DB 1 CEFLVKEVTKLIDNNKTEKEILDADF 25

RESULT 11

AAR70773

ID AAR70773 standard; peptide; 22 AA.

XX AAR70773;

XX 30-AUG-1995 (first entry)

XX Saposin-C neurotrophic peptide.

XX Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW adrenal leukodystrophy.

XX Homo sapiens.

XX WO9503821-A.

XX 09-FEB-1995.

XX 28-JUL-1994; 94WO-US08453.

XX 30-JUL-1993; 93US-0100247.

XX 21-APR-1994; 94US-0232513.

XX (OBRI/) OBRIEN J S.

XX Kishimoto Y, Obrien JS;

XX WPI; 1995-082029/11.

XX Stimulating neural cell out-growth and myelination - with  
PT pro-saposin, saposin C or new neurotrophic peptide(s) from  
PT cytokine(s), for treating nervous system diseases

PS Disclosure; Page 30; 50pp; English.

XX The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neuroepithelial cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosaposin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.

XX Sequence 22 AA;

Query Match 52.6%; Score 111; DB 16; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.6e-07;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29

DB 1 CEFLVKEVTKLIDNNKTEKEIL 22

RESULT 12

AAW30013

ID AAW30013 standard; peptide; 22 AA.

XX AAW30013;

XX 14-APR-1998 (first entry)

XX Prosaposin-derived peptide 22-mer.

XX Human; prosaposin; neural disorder; demyelination disorder;  
KW neural cell death; inhibition; myelination; neurite outgrowth;  
KW neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy;  
KW polynuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus.  
XX Homo sapiens.  
XX OS  
XX PN WO9732895-A1.  
XX PD 12-SEP-1997.  
XX PF 05-MAR-1997; 97WO-US04143.  
XX PR 05-MAR-1996; 96US-0611307.  
XX PA (REGC ) UNIV CALIFORNIA.  
XX PI O'Brien JS;  
XX WPI; 1997-470538/43.  
XX Prosaposin-derived peptide - useful for therapy of neural or  
PT demyelination disorders in neural tissue  
XX  
XX Claim 9; Page 52; 69pp; English.  
CC The present sequence represents a prosaposin-derived peptide. A method  
CC has been developed of alleviating or preventing neuropathic pain in a  
CC subject, comprising administering an effective amount of an active  
CC fragment of prosaposin to the subject. The prosaposin-derived peptide  
CC is useful for therapy of neural or demyelination disorders in neural  
CC tissue. It can be used to stimulate neurite outgrowth, inhibit neural  
CC cell death, promote myelination or inhibit demyelination. The method  
CC is used to alleviate neuropathic pain resulting from a peripheral nerve  
CC disorder, such as neuroma, nerve compression, crush or stretch and  
CC incomplete nerve transection, mononeuropathy or polynuropathy.  
CC Alternatively the neuropathic pain results from a disorder of the  
CC dorsal root ganglia, spinal cord, brainstem, thalamus or cortex.  
XX  
XX Sequence 22 AA;  
SQ  
Query Match 52.6%; Score 111; DB 18; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CEFVLKREVTKLIDNNKTEKIL 29  
Db 1 CEFVLKREVTKLIDNNKTEKIL 22  
RESULT 13  
AAW66127  
ID AAW66127 standard; peptide; 22 AA.  
XX AC AAW66127;  
XX DT 17-NOV-1998 (first entry)  
XX DE Prosaposin receptor agonist #1.  
XX KW prosaposin; receptor agonist; neuropathic pain; neurite outgrowth;  
KW neural cell death; nerve disorder; side effect.  
XX Synthetic.  
OS Homo sapiens.  
XX OS  
XX PN WO9839357-A1.  
XX PD 11-SEP-1998.  
XX PF 11-SEP-1997; 97WO-US16062.

PR 05-MAR-1997; 97WO-US04143.  
XX (REGC ) UNIV CALIFORNIA.  
XX PI O'Brien JS;  
XX WPI; 1998-495790/42.  
DR N-PSDB; AAV07664.  
XX  
PT Use of prosaposin receptor agonists - for alleviating neuropathic  
PT pain, inhibiting sensory or motor neuropathy, or inhibiting neural  
PT cell death  
XX  
XX Claim 3; Page 2; 67pp; English.  
XX  
CC The invention relates to prosaposin receptor agonists. Also claimed  
CC are: (1) methods for alleviating neuropathic pain or inhibiting the  
CC onset of neuropathic pain, comprising administering a prosaposin receptor  
CC agonist; (2) inhibiting sensory or motor neuropathy, comprising  
CC contacting neuronal cells with a composition comprising a prosaposin  
CC receptor agonist; (3) methods for stimulating neurite outgrowth,  
CC inhibiting neural cell death, promoting myelination, or inhibiting  
CC demyelination comprising contacting neuronal cells with a composition  
CC comprising a prosaposin receptor agonist which has 14-50 amino acids and  
CC comprises the sequence of a prosaposin derived protein. The processes  
CC may be used for treatment of neuropathic pain resulting from peripheral  
CC nerve disorders (e.g. neuroma, nerve compression, nerve crush, nerve  
CC stretch, incomplete nerve transection, mononeuropathy or polynuropathy)  
CC or disorders of dorsal root ganglia, the spinal cord, the brainstem, the  
CC thalamus or the cortex. The receptor agonists do not cause undesirable  
CC side effects. The present sequence represents a specifically claimed  
CC prosaposin receptor agonist.  
XX  
XX Sequence 22 AA;  
SQ  
Query Match 52.6%; Score 111; DB 19; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CEFVLKREVTKLIDNNKTEKIL 29  
Db 1 CEFVLKREVTKLIDNNKTEKIL 22  
RESULT 14  
AAW85656  
ID AAW85656 standard; Peptide; 22 AA.  
XX AC AAW85656;  
XX DT 19-JUL-1999 (first entry)  
XX DE Prosaposin receptor agonist.  
XX KW Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
OS Homo sapiens.  
XX OS  
XX PN WO9912559-A1.  
XX PD 18-MAR-1999.

XX 09-SEP-1998; 98WO-US19216.  
XX  
XX  
PR 04-JUN-1998; 98US-0088129.  
PR 09-SEP-1997; 97US-0058352.  
XX  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
XX  
XX O'brien JS;  
PI  
XX  
DR WPI; 1999-229139/19.  
PT  
PT use of prosaposin receptor agonist  
XX  
XX  
PS Claim 7; Page 66; 90pp; English.

XX Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
CC to generate saposins A, B, C and D, all of which are similar to each  
CC other and have a similar placement of six cysteines, a glycosylation  
CC site and conserved proline residues. Prosaposin, saposin C and  
CC prosaposin derived peptides (prosapptides), have therapeutic  
CC applications in promoting recovery after toxic, traumatic, myocardial  
CC ischaemic, degenerative and inherited lesions to the peripheral and  
CC central nervous system. Prosaposin receptor agonists (PRAS)  
CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
CC members which inhibit caspases, thereby inhibiting apoptosis. An  
CC additional mechanism whereby PRAS inhibit apoptosis is by blocking  
CC activation of JNK, a proapoptotic signaling component. Within  
CC several minutes after binding to the receptor, PRAS block JNK  
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
CC apoptosis. The method can be used for inhibiting apoptosis which is  
CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. This peptide corresponds to amino acids 8 to 29 of  
CC human saposin C (See AAW85553) and acts as a prosaposin receptor  
CC agonist.

XX Sequence 22 AA;

Query Match 52.6%; Score 111; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLYKEVTKLIDNNKTEKEIL 29  
Db 1 CEFLYKEVTKLIDNNKTEKEIL 22

RESULT 15  
AAB67305  
ID AAB67305 standard; Peptide; 22 AA.

XX AAB67305;

XX  
XX  
DT 20-APR-2001 (first entry)

XX Peptide #5.

XX Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.

OS Homo sapiens.  
XX  
XX  
PN EP1072609-A2.  
XX  
XX  
PD 31-JAN-2001.

XX 30-JUN-2000; 2000EP-0305504.

XX 30-JUN-1999; 99JP-0185155.

XX (SAKA/) SAKANAKA M.

XX (TANA/) TANAKA J.

XX (SATO/) SATO K.

XX Sakanaka M, Tanaka J, Sato K, Morita E, Sadamoto Y;

XX WPI; 2001-204263/21.

XX Use of prosaposin-related peptides or derivatives as cytoprotective  
PT agents, for suppressing apoptosis or apoptosis-like cell death -  
XX  
XX Disclosure; Page 28; 41pp; English.

XX The present invention relates to use of a prosaposin-related peptide  
CC or derivative, in the production of a medicament for use in  
CC preventing or delaying cell death, or in promoting the expression  
CC of cell death supporting gene product Bcl-XL. The invention is  
CC useful for preventing the death of cells e.g. brain cells,  
CC neurons and cardiac muscle cells, in vitro or ex vivo.

XX Sequence 22 AA;

Query Match 52.6%; Score 111; DB 22; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLYKEVTKLIDNNKTEKEIL 29

Db 1 CEFLYKEVTKLIDNNKTEKEIL 22

Search completed: June 2, 2003, 14:15:44  
Job time : 32.2821 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 14.359 Seconds  
(without alignments)  
267.803 Million cell updates/sec

Title: US-09-780-438C-1

Perfect score: 211

Sequence: 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFKMCKSLP 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	527	1	SAHUP
2	172	81.5	80	2	saposin-C - bovine
3	119	56.4	81	2	glucosylceramide b
4	93	44.1	554	1	saposin precursor
5	85	40.3	557	1	saposin precursor
6	80	37.9	496	2	aspartic proteinas
7	78	37.0	428	2	cynarase (EC 3.4.2
8	78	37.0	474	2	cyprosin (EC 3.4.2
9	78	37.0	965	2	p109 protein - sil
10	75	35.5	508	2	aspartic proteinas
11	74	35.1	280	2	aspartic proteinas
12	74	35.1	506	2	probable aspartic
13	74	35.1	513	2	aspartic proteinas
14	72	34.1	292	2	T11446
15	72	34.1	322	2	S41400
16	70	33.2	506	2	F86253
17	69	32.7	509	2	hypothetical prote
18	69	32.7	509	2	cyprosin (EC 3.4.2
19	68	32.2	513	2	T09739
20	67.5	32.0	314	2	T15674
21	65	30.8	509	2	JC7272
22	64	30.3	3228	2	T21381
23	63.5	30.1	330	2	B71625
24	63	29.9	123	2	S75382
25	62.5	29.6	139	2	F97080
26	62.5	29.6	226	2	G96975
27	62	29.4	213	2	T46069
28	61	28.9	506	2	S71591
29	58.5	27.7	1732	2	G84664

30	58	27.5	137	2	B64411
31	57.5	27.3	209	2	A71800
32	57.5	27.3	217	2	T48201
33	57	27.0	332	2	T00657
34	57	27.0	428	2	D84615
35	57	27.0	845	2	D97163
36	56.5	26.8	155	2	C64718
37	56.5	26.8	261	2	E85439
38	56.5	26.8	375	2	A71625
39	56.5	26.8	774	2	JC2299
40	56.5	26.8	1048	2	C86189
41	56	26.5	281	2	A97017
42	56	26.5	869	2	F97126
43	56	26.5	1232	2	T47993
44	55.5	26.3	1232	2	D64413
45	55	26.1	105	2	F71128

#### ALIGNMENTS

#### RESULT 1

SAHUP

saposin precursor [validated] - human

N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon  
ein (SAP); sphingolipid activator protein A2; sulfatide sulfatase activator protein

N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence\_revision 17-Nov-1995 #text\_change 08-Dec-2000

C:Accession: JX0061; A57368; A42003; B42003; C42003; D42003; A30367; S34740; S36140;  
0226; I37265; I37264

R:Nakano, T.; Sandhoff, K.; Stuenkel, J.; Christomanou, H.; Suzuki, K.

J. Biochem. 105, 152-154, 1989

A:Title: Structure of full-length cDNA coding for sulfatide activator, a Co-beta-glyc

A:Reference number: JX0061; MUID:89255151; PMID:2498298

A:Accession: JX0061

A:Molecule type: mRNA

A:Residues: 1-527 <NA>

A:Cross-references: GB:D00422; NID:g220063; PIDN:BAA00321.1; PID:g220064

A:Note: alternative splice form 1

A:Accession: A57368

A:Molecule type: mRNA

A:Residues: 1-259,263-527 <NA2>  
A:Cross-references: GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59494.1; PID:g337756

A:Note: alternative splice form 2

R:Rorman, E.G.; Scheinker, V.; Grabowski, G.A.

A;Cross-references: GB:J03077; NID:g183230; PIDN:AAA52560.1; PID:g183231  
A;Note: alternative splice form 2  
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Biochem. Biophys. 304, 110-116, 1993  
A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor  
A;Reference number: S34740; MUID:93311991; PMID:8333276  
A;Accession: S34740  
A;Molecule type: protein  
A;Residues: 17-24;165-172;180-189;301-305 <HIR>  
R;Tynnelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M. FEBS Lett. 330, 8-12, 1993  
A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.  
A;Reference number: S36140; MUID:93380576; PMID:8370464  
A;Accession: S36140  
A;Molecule type: protein  
A;Residues: 'XX', 62, 'X', 64-65, 'X', 67-79, 'X', 81-84 <TY>  
A;Note: saposin A  
A;Accession: S36141  
A;Molecule type: protein  
A;Residues: 'XXX', 413-414, 'X', 416-428, 'X', 430-434 <TY2>  
A;Note: saposin D  
R;Holtzschmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K. J. Biol. Chem. 266, 7556-7560, 1991  
A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs and  
A;Reference number: S36988; MUID:91210267; PMID:2019586  
A;Accession: S36988  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-527 <HO2>  
A;Cross-references: EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PID:g337760  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative splicing  
A;Accession: S36989  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-259, 263-527 <HO2>  
A;Cross-references: EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PID:g337765  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative splicing  
A;Accession: S36990  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-259, 261-527 <HO3>  
A;Cross-references: EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PID:g337767  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative splicing  
R;Kondoh, K.; Hinenio, T.; Sano, A.; Kakimoto, Y. Biochem. Biophys. Res. Commun. 181, 286-292, 1991  
A;Title: Isolation and characterization of prosaposin from human milk.  
A;Reference number: PS0330; MUID:92068206; PMID:1958198  
A;Accession: PS0330  
A;Molecule type: protein  
A;Residues: 17-24, 'X', 26 <KON>  
A;Experimental source: milk  
R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990  
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosylation  
A;Reference number: A35985; MUID:90207231; PMID:2320574  
A;Accession: A35985  
A;Molecule type: mRNA  
A;Residues: 213-221 <KRE>  
A;Cross-references: GB:M32221  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-259, 263-527 <KR2>  
A;Cross-references: GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:g337762  
A;Experimental source: lymphoblast  
A;Accession: C35985  
A;Molecule type: mRNA  
A;Residues: 213-216, 'I', 218-221 <KR3>  
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; the  
R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.

Eur. J. Biochem. 192, 709-714, 1990  
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein  
A;Reference number: S13195; MUID:91006165; PMID:2209618  
A;Accession: S13196  
A;Molecule type: protein  
A;Residues: 195-259, 263-277 <FUE>  
R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y. Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989  
A;Title: Saposin A: second cerebroside activator protein.  
A;Reference number: A32784; MUID:89240739; PMID:2717620  
A;Accession: A32784  
A;Molecule type: protein  
A;Residues: 60-84;86-107;109-119;125-134 <MOR>  
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L. Science 241, 1098-1101, 1988  
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same gene  
A;Reference number: A41240; MUID:88321660; PMID:2842863  
A;Accession: A41240  
A;Molecule type: mRNA  
A;Residues: 'GSSR', 18-259, 263-299, 'D', 301-302, 'D', 304-527 <OAB>  
A;Cross-references: GB:J03086  
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 84, 8632-8656, 1987  
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein  
A;Reference number: S02289; MUID:88068647; PMID:2825202  
A;Accession: S02289  
A;Status: significant sequence differences  
A;Molecule type: mRNA  
A;Cross-references: EMBL:J03015  
A;Note: this sequence corrected by A41240  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 369, 1361-1365, 1988  
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein  
A;Reference number: S02028; MUID:89207118; PMID:3242555  
A;Accession: S02028  
A;Molecule type: protein  
A;Residues: 195-259, 263-276 <KLE>  
R;Fuerst, W.; Machleidt, W.; Sandhoff, K. Biol. Chem. Hoppe-Seyler 369, 317-328, 1988  
A;Title: The precursor of sulfatide activator protein is processed to three different  
A;Reference number: S00813; MUID:89000190; PMID:3048308  
A;Accession: S00813  
A;Molecule type: protein  
A;Residues: 410-487 <FU2>  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987  
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurring  
A;Reference number: S00226; MUID:88163077; PMID:3442600  
A;Accession: S00226  
A;Molecule type: protein  
A;Residues: 314-393 <KL2>  
R;Vaccaro, A.M.; Salvio, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Sicilia J. Biol. Chem. 270, 9953-9960, 1995  
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide bonds  
A;Reference number: A57297; MUID:95247790; PMID:7730378  
A;Contents: annotation; disulfide bonds; glycosylation  
R;Holtzschmidt, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K. FEBS Lett. 280, 267-270, 1991  
A;Title: The organization of the gene for the human cerebroside sulfate activator protein  
A;Reference number: I37264; MUID:91192146; PMID:2013321  
A;Accession: I37265  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 59-125 <RES>  
A;Cross-references: EMBL:X57107; NID:g30234; PIDN:CAA40391.1; PID:g30235  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 307-516 <RE2>  
A;Cross-references: EMBL:X57108; NID:g30232; PIDN:CAA40392.1; PID:g1565257  
A;Note: sequence revised relative to PID:g30233 (corrected coding region)  
C;Genetics:



F;194-276/Product: saposin B #status predicted <SAB1>  
F;309-400/Domain: saposin B repeat homology <SAP3>  
F;313-392/Product: saposin C #status predicted <SAPC>  
F;434-525/Domain: saposin repeat homology <SAP4>  
F;440-517/Product: saposin D #status predicted <SAPD>  
F;63-138,66-132,94-106,197-273,200-267,229-240,317-390,  
F;80,214,334,379,459/Binding site: carbohydrate (Asn) #status predicted.

Query Match 40.3%; Score 85; DB 1; Length 557;  
Best Local Similarity 45.9%; Pred. No. 0.03; Mismatches 12; Indels 0; Gaps 0;

Matches 17; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 YCEVCEFLVKEVTKLIDNNKTEKELDAFDKMGSKLP 40  
:||||: || : : : ||:|||| : |||||  
Db 441 FCEVCKLVLYLEHNLEKNTKEILLAALEKGCFLP 477

## RESULT 6

JS0732

Aspartic proteinase (EC 3.4.23.-) - rice

C;Species: Oryza sativa (rice)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 20-Jun-2000

C;Accession: JS0732; PC4079

R;Hashimoto, H.; Nishi, R.; Uchimiya, H.; Kato, A.

Submitted to JIPID, August 1992

A;Reference number: JS0732

A;Accession: JS0732

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-496 &lt;HAS&gt;

A;Cross-references: DDBJ:D12777; NID:g218142; PIDN:BAA02242.1; PID:g218143

A;Experimental source: strain Yamahoushi

R;Asakura, T.; Abe, K.; Arai, S.

BioSci. Biotechnol. Biochem. 59, 1793-1794, 1995

A;Title: Evidence for the occurrence of multiple aspartic proteinases in rice seeds.

A;Reference number: PC4079; MUID:96014423; PMID:8520124

A;Accession: PC4079

A;Molecule type: mRNA

A;Residues: 189-468 &lt;ASA&gt;

A;Cross-references: DDBJ:D12777

A;Experimental source: seeds

C;Comment: This is a multigene family.

C;Genetics: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a

C;Gene: ap

C;Superfamily: oryzasin; saposin repeat homology

C;Keywords: aspartic proteinase; hydrolase; seed

F;308-353/Domain: saposin repeat homology #status atypical &lt;SAP1&gt;

F;362-407/Domain: saposin repeat homology #status atypical &lt;SAP2&gt;

F;95,282/Active site: Asp #status predicted

F;95,282/Active site: Asp #status predicted

Query Match 37.9%; Score 80; DB 2; Length 496;

Best Local Similarity 37.5%; Pred. No. 0.1;

Matches 15; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 SDYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMGSKLP 40  
||| ||| : : : |||: ||| : |||: |||

Db 366 SDAMCSVCMAVVMQNIQNETEENIINVDKLCERLP 405

## RESULT 7

S47096

cynarase (EC 3.4.23.-) - cardoon

C;Species: Cynara cardunculus (cardoon)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 29-Aug-1997

C;Accession: S47096

R;Cordeiro, M.C.; Xue, Z.T.; Pietrzak, M.; Pais, M.S.; Brodelius, P.

submitted to the EMBL Data Library, November 1992

A;Description: Tissue specific expression of cynarase (s) genes in flowers of Cynara card

A;Reference number: S47096

A;Accession: S47096

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-428 &lt;COR&gt;

A;Cross-references: EMBL:X69193

C;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent

C;Superfamily: oryzasin; saposin repeat homology

C;Keywords: aspartic proteinase; hydrolase

F;236-281/Domain: saposin repeat homology #status atypical &lt;SAP1&gt;

F;290-339/Domain: saposin repeat homology #status atypical &lt;SAP2&gt;

F;23,210/Active site: Asp #status predicted

Query Match 37.0%; Score 78; DB 2; Length 428;

Best Local Similarity 35.9%; Pred. No. 0.15;

Matches 14; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 DVCVCEFLVKEVTKLIDNNKTEKELDAFDKMGSKLP 40  
| | | | : : : | | | | : : : | | | |

Db 299 DEMCTMCQMAVVMQNIQNETEENIINVDKLCERLP 337

## RESULT 8

T12049

CYP109 protein - silkworm

N;Alternate names: cynarase

C;Species: Cynara cardunculus (cardoon)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000

C;Accession: T12049

R;Cordeiro, M.C.; Xue, Z.T.; Pietrzak, M.; Pais, M.S.; Brodelius, P.E.

Plant Mol. Biol. 24, 733-741, 1994

A;Title: Isolation and characterization of a cDNA from flowers of Cynara cardunculus

A;Reference number: Z17395; MUID:94250836; PMID:8193298

A;Accession: T12049

A;Status: preliminary;

A;Molecule type: mRNA

A;Residues: 1-474 &lt;COR&gt;

A;Cross-references: EMBL:X69193; NID:g499015; PIDN:CAA48939.1; PID:g509163

A;Experimental source: flower

C;Superfamily: oryzasin; saposin repeat homology

C;Keywords: aspartic proteinase; hydrolase

Query Match 37.0%; Score 78; DB 2; Length 474;

Best Local Similarity 35.9%; Pred. No. 0.17;

Matches 14; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 DVCVCEFLVKEVTKLIDNNKTEKELDAFDKMGSKLP 40  
| | | | : : : | | | | : : : | | | |

Db 345 DEMCTMCQMAVVMQNIQNETEENIINVDKLCERLP 383

## RESULT 9

T00207

P109 protein - silkworm

C;Species: Bombyx mori (silkworm)

C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 21-Jul-2000

C;Accession: T00207

R;Rambunan, J.; Chang, P.K.; Li, H.; Natori, M.

Gene 212, 287-293, 1998

A;Title: Molecular cloning of a cDNA encoding a silkworm protein which contains the c

A;Reference number: Z14124; MUID:98278844; PMID:9611271

A;Accession: T00207

A;Status: preliminary;

A;Molecule type: mRNA

A;Residues: 1-965 &lt;TAM&gt;

A;Cross-references: EMBL:AB08449; NID:g2575864; PIDN:BAA23126.1; PID:g2575865

C;Superfamily: saposin repeat homology

F;778-870/Domain: saposin repeat homology &lt;SAP3&gt;

Query Match 37.0%; Score 78; DB 2; Length 965;

Best Local Similarity 38.9%; Pred. No. 0.34;

Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 5 CEVCEFLVKEVTKLIDNNKTEKELDAFDKMGSKLP 40  
| | | | : | | | : | | | : | | |

Db 877 CAVCEVVMVAVKVLNKLNRNIVHIEKSCGLLP 912

## RESULT 10

S19697  
aspartic proteinase (EC 3.4.23.-) precursor - barley  
C:Species: Hordeum vulgare (barley)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Jun-1999  
C:Accession: S19697  
R:Runeberg-Roos, P.; Toermaekangas, K.; Oestman, A.  
Eur. J. Biochem. 202, 1021-1027, 1991  
A:Title: Primary structure of a barley-grain aspartic proteinase. A plant aspartic prote  
A:Reference number: S19697; MUID:92111473; PMID:1722454  
A:Accession: S19697  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-508 <RUN>  
A:Cross-references: EMBL:X56136; NID:g18903; PIDN:CAA39602.1; PID:g18904  
C:Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a  
C:Superfamily: oryzasin; saposin repeat homology  
C:Keywords: aspartic proteinase; hydrolase  
F:315-360/Domain: saposin repeat homology #status atypical <SAP1>  
F:369-419/Domain: saposin repeat homology #status atypical <SAP2>  
F:102,289/Active site: Asp #status predicted

Query Match 35.5%; Score 75; DB 2; Length 508;

Best Local Similarity 35.0%; Pred. No. 0.4;

Matches 14; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

Db 378 ADPCACEMAVVWQNLQAKNTQDILLDVNQLCNRLP 417

## RESULT 11

PC4080  
aspartic proteinase (EC 3.4.23.-) L5 - rice (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 29-Aug-1997  
C:Accession: PC4080  
R:Asakura, T.; Abe, K.; Arai, S.  
Biosci. Biotechnol. Biochem. 59, 1793-1794, 1995  
A:Title: Evidence for the occurrence of multiple aspartic proteinases in rice seeds.  
A:Reference number: PC4079; MUID:96014423; PMID:8520124  
A:Accession: PC4080  
A:Molecule type: mRNA  
A:Residues: 1-280 <ASA>  
A:Cross-references: DDBJ:D12777  
A:Experimental source: seeds  
C:Comment: This is a multigene family.  
C:Accession: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a

C:Genetics:

A:Gene: ap

C:Superfamily: oryzasin; saposin repeat homology

C:Keywords: aspartic proteinase; hydrolase; seed

F:120-165/Domain: saposin repeat homology #status atypical <SAP1>

F:174-219/Domain: saposin repeat homology #status atypical <SAP2>

F:94/Active site: Asp #status predicted

Query Match

Best Local Similarity 35.1%; Score 74; DB 2; Length 280;

Matches 14; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

Db 178 SDSLCTACEMSVWVWQNLQRLNQHNTRELLIQADQLCERLP 217

Db 178 SDSLCTACEMSVWVWQNLQRLNQHNTRELLIQADQLCERLP 217

Db 178 SDSLCTACEMSVWVWQNLQRLNQHNTRELLIQADQLCERLP 217

Db 178 SDSLCTACEMSVWVWQNLQRLNQHNTRELLIQADQLCERLP 217

Db 178 SDSLCTACEMSVWVWQNLQRLNQHNTRELLIQADQLCERLP 217

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Db 178 SDSLCTACEMSVWVWQNLQRLNQHNTRELLIQADQLCERLP 217

R:D'Hondt, K.; Stack, S.; Gutteridge, S.; Vandekerckhove, J.; Krebbers, E.; Gal, S.  
Plant Mol. Biol. 33, 187-192, 1997  
A:Title: Aspartic proteinase genes in the Brassicaceae Arabidopsis thaliana and Brass  
A:Reference number: Z16211; MUID:97188586; PMID:9037171  
A:Accession: T07915  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-506 <DHO>  
A:Cross-references: EMBL:U55032; NID:g1326164; PIDN:AAB03108.1; PID:g1326165  
C:Genetics:  
A:Introns: 116/3; 137/1; 168/3; 206/2; 262/3; 276/1; 297/3; 335/3; 357/2; 409/3; 449/3  
C:Superfamily: oryzasin; saposin repeat homology  
C:Keywords: aspartic proteinase; hydrolase

Query Match 35.1%; Score 74; DB 2; Length 506;

Best Local Similarity 33.3%; Pred. No. 0.52;

Matches 13; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 2 DVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

Db 377 DACSACEMAVVWQNLQRLNQHNTRELLIQADQLCERLP 415

Db 377 DACSACEMAVVWQNLQRLNQHNTRELLIQADQLCERLP 415

Db 377 DACSACEMAVVWQNLQRLNQHNTRELLIQADQLCERLP 415

Db 377 DACSACEMAVVWQNLQRLNQHNTRELLIQADQLCERLP 415

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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:13 ; Search time 7.17949 Seconds  
(without alignments)  
231.082 Million cell updates/sec

Title: US-09-780-438c-1

Perfect score: 211

Sequence: 1 SDVYCEVCEFLVREVKLIDNNKTEKILDAFDKMGSKLP 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	211	100.0	524	1	SAP_HUMAN
2	175	82.9	525	1	SAP_BOVIN
3	119	56.4	81	1	SAP_CAVPO
4	108	51.2	518	1	SAP_CHICK
5	93	44.1	554	1	SAP_RAT
6	85	40.3	557	1	SAP_MOUSE
7	80	37.9	496	1	ASPR_ORYSA
8	75	35.5	508	1	ASPR_HORVU
9	69	32.7	509	1	APRI_ORYSA
10	68	32.2	513	1	ASPR_CUCPE
11	64	30.3	473	1	CYPL_CYNCA
12	58.5	27.7	495	1	MATK_TORCL
13	58	27.5	137	1	Y890_MERJA
14	57.5	27.3	209	1	YF87_HELPJ
15	56.5	26.8	209	1	YF87_HELPJ
16	55	26.1	105	1	Y795_PYRHO
17	55	26.1	313	1	Y085_CABEL
18	55	26.1	389	1	O85C_DROME
19	54	25.6	173	1	ARPL_DROME
20	54	25.6	213	1	KITH_MYCGE
21	53	25.1	196	1	V17_BPT7
22	53	25.1	542	1	TCPE_CABEL
23	52.5	24.9	92	1	Y450_HAEIN
24	52	24.6	449	1	ARP3_YEAST
25	51.5	24.4	455	1	VNSL_BMDNV
26	51.5	24.4	524	1	E2BD_MOUSE
27	51.5	24.4	740	1	FAS_PNECA
28	51	24.2	91	1	RR19_NICBI
29	51	24.2	91	1	RR19_TORAC
30	51	24.2	105	1	YF40_PYRAB
31	51	24.2	129	1	NKL_FIG
32	51	24.2	392	1	MT04_CAMJE
33	51	24.2	453	1	5HT1_APLCA

34 51 24.2 656 1 V091\_FOWPV  
35 51 24.2 657 1 YG66\_YEAST  
36 50.5 23.9 97 1 PEPN\_ENTHI  
37 50.5 23.9 332 1 YC56\_PASMU  
38 50.5 23.9 926 1 UBP4\_YEAST  
39 50.5 23.9 956 1 SYI\_AQUAE  
40 50 23.7 202 1 T2M2\_METTF  
41 50 23.7 299 1 MRAW\_MYCPU  
42 50 23.7 377 1 PSPB\_MOUSE  
43 50 23.7 515 1 MATK\_CEDAT  
44 50 23.7 515 1 MATK\_PICGL  
45 50 23.7 515 1 MATK\_PICRU

072896 fowlpox vir  
P53165 saccharomyc  
Q07831 entamoeba h  
Q8clh5 pasteurella  
P32571 saccharomyc  
O86651 aquifex ae  
P29566 methanobact  
Q98q75 mycoplasma  
P50405 mus musculu  
Q9mv56 cedrus atla  
O63070 picea glauc  
O63071 picea ruben

## ALIGNMENTS

RESULT 1  
SAP\_HUMAN STANDARD; PRT; 524 AA.  
AC P07602: P07292; P15793; P78538; P78546; P78547; Q92741; Q92742;  
AC Q92740; Q92739; P78541; P78558;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Proactivator polypeptide precursor [Contains: Saposin A (Protein A);  
DE Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside  
DE sulfate activator) (CSact) (Dispersin) (Sulfatide/GMI activator);  
DE Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase  
DE activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D  
DE (Protein C) (Component C)].  
DE PSAP.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=90129043; PubMed=2515150;  
RA Norman E.G., Grabowski G.A.;  
RT "Molecular cloning of a human co-beta-glucosidase cDNA: evidence that  
RT four sphingolipid hydrolase activator proteins are encoded by single  
RT genes in humans and rats.";  
RL Genomics 5:486-492(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89255151; PubMed=2498298;  
RA Nakano T., Sandhoff K., Stuenkel J., Christomanou H., Suzuki K.;  
RT "Structure of full-length cDNA coding for sulfatide activator, a  
RT Co-beta-glucosidase and two other homologous proteins: two alternate  
RT forms of the sulfatide activator.";  
RL J. Biochem. 105:152-154(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Eye, and Skin;  
RA Strausberg R.;  
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 59-125 AND 304-513 FROM N.A.  
RX TISSUE=Brain;  
RT MEDLINE=91192146; PubMed=2013321;  
RA Holtschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D.,  
RA Suzuki K.;  
RT "The organization of the gene for the human cerebroside sulfate  
RT activator protein.";  
RL FEBS Lett. 280:267-270(1991).  
RN [5]  
RP SEQUENCE OF 164-524 FROM N.A.  
RX MEDLINE=88068647; PubMed=2825202;  
RA Dewji N.N., Wenger D.A., O'Brien J.S.;  
RT "Nucleotide sequence of cloned cDNA for human sphingolipid activator  
RT protein 1 precursor.";

Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).  
[6]  
PARTIAL SEQUENCE OF 60-142.  
MEDLINE-89240739; PubMed-2717620;  
RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,  
RA Kishimoto Y.;  
RT "Saposin A: second cerebroside activator protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).  
[7]  
SEQUENCE OF 195-263 FROM N.A.  
RA MEDLINE-86130593; PubMed-2868718;  
RX MEDLINE-86130593; PubMed-2868718;  
RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,  
RA Hill F., O'Brien J.S.;  
RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),  
RT the sulfatide-sulfatase activator.";  
RL Biochem. Biophys. Res. Commun. 134:989-994(1986).  
[8]  
SEQUENCE OF 195-274.  
RA TISSUE-Urine;  
RX MEDLINE-91006165; PubMed-2209618;  
RA Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;  
RT "The complete amino-acid sequences of human ganglioside GM2 activator  
RT protein and cerebroside sulfate activator protein.";  
RL Eur. J. Biochem. 192:709-714(1990).  
[9]  
SEQUENCE OF 195-274.  
RA MEDLINE-89207118; PubMed-3242555;  
RX MEDLINE-89207118; PubMed-3242555;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence of the naturally occurring A2 activator  
RT protein for enzymic sphingomyelin degradation: identity to the  
RT sulfatide activator protein (SAP-1).";  
RL Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).  
[10]  
SEQUENCE OF 311-390.  
RA MEDLINE-88163077; PubMed-3442600;  
RX MEDLINE-88163077; PubMed-3442600;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence and carbohydrate content of the  
RT naturally occurring glucosylceramide activator protein (A1 activator)  
RT absent from a new human Gaucher disease variant.";  
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).  
[11]  
SEQUENCE OF 407-484.  
RA MEDLINE-89000190; PubMed-3048308;  
RX MEDLINE-89000190; PubMed-3048308;  
RA Furst W., Machleidt W., Sandhoff K.;  
RT "The precursor of sulfatide activator protein is processed to three  
RT different proteins.";  
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).  
[12]  
PARTIAL SEQUENCE OF 405-484.  
RA MEDLINE-89025876; PubMed-2845979;  
RX MEDLINE-89025876; PubMed-2845979;  
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;  
RT "Saposin D: a sphingomyelinase activator.";  
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).  
[13]  
SEQUENCE OF 17-26.  
RA TISSUE-Milk;  
RX MEDLINE-92068206; PubMed-1958198;  
RA Kondoh K., Hinenio T., Sano A., Kakimoto Y.;  
RT "Isolation and characterization of prosaposin from human milk.";  
RL Biochem. Biophys. Res. Commun. 181:286-292(1991).  
[14]  
PARTIAL SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.  
RA TISSUE-Urine;  
RX MEDLINE-20032116; PubMed-10562467;  
RA Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.,  
RA Waring A.J., To T., Fluharty C.B., Faull K.F.;  
RT "Preparation of the cerebroside sulfate activator (CSAct or saposin B)  
RT from human urine.";  
RL Mol. Genet. Metab. 68:391-403(1999).  
[15]  
STRUCTURE OF CARBOHYDRATE ON ASN-215.  
RA MEDLINE-21110404; PubMed-11180632;  
RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,

RA Stevens R.L., Fluharty C.B., Fluharty A.L.;  
RT "Structure of the asparagine-linked sugar chains of porcine kidney and  
RT human urine cerebroside sulfate activator protein.";  
RL J. Mass Spectrom. 35:1416-1424(2000).  
[16]  
MASS SPECTROMETRY.  
RA TISSUE-Urine;  
RX MEDLINE-99441404; PubMed-10510427;  
RA Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,  
RA Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,  
RA Fluharty C.B., Fluharty A.L.;  
RT "Cerebroside sulfate activator protein (Saposin B): chromatographic  
RT and electrospray mass spectrometric properties.";  
RL J. Mass Spectrom. 34:1040-1054(1999).  
[17]  
VARIANT MLD ILE-217.  
RA MEDLINE-90147748; PubMed-2302219;  
RX MEDLINE-90147748; PubMed-2302219;  
RA Rafi M.A., Zhang X.-L., Degala G., Wenger D.A.;  
RT "Detection of a point mutation in sphingolipid activator protein-1  
RT mRNA in patients with a variant form of metachromatic  
RT leukodystrophy.";  
RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).  
[18]  
SEQUENCE FROM N.A., AND VARIANT MLD ILE-217.  
RA MEDLINE-90207231; PubMed-2320574;  
RX MEDLINE-90207231; PubMed-2320574;  
RA O'Brien J.S.;  
RT "Characterization of a mutation in a family with saposin B  
RT deficiency: a glycosylation site defect.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).  
[19]  
VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RA MEDLINE-91210267; PubMed-2019586;  
RX MEDLINE-91210267; PubMed-2019586;  
RA Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,  
RA Suzuki K.;  
RT "Sulfatide activator protein. Alternative splicing that generates  
RT three mRNAs and a newly found mutation responsible for a clinical  
RT disease.";  
RL J. Biol. Chem. 266:7556-7560(1991).  
[20]  
VARIANT GAUCHER PHE-388.  
RA MEDLINE-91285107; PubMed-2060627;  
RX MEDLINE-91285107; PubMed-2060627;  
RA Schnabel D., Schroeder M., Sandhoff K.;  
RT "Mutation in the sphingolipid activator protein 2 in a patient with a  
RT variant of Gaucher disease.";  
RL FEBS Lett. 284:57-59(1991).  
[21]  
REVIEW ON MLD VARIANTS.  
RA MEDLINE-95170731; PubMed-7866401;  
RX MEDLINE-95170731; PubMed-7866401;  
RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;  
RT "Molecular genetics of metachromatic leukodystrophy.";  
RL Hum. Mutat. 4:233-242(1994).  
CC -!- FUNCTION: The lysosomal degradation of sphingolipids takes place  
CC by the sequential action of specific hydrolases. Some of these  
CC enzymes require specific low-molecular mass, non-enzymic proteins:  
CC the sphingolipid activator proteins (coproteins).  
CC -!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of  
CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and  
CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).  
CC Saposin C apparently acts by combining with the enzyme and acidic  
CC lipid to form an activated complex, rather than by solubilizing  
CC the substrate.  
CC -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-  
CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1  
CC gangliosides by beta-galactosidase (EC 3.2.1.23) and  
CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).  
CC Saposin B forms a solubilizing complex with the substrates of the  
CC sphingolipid hydrolases.  
CC -!- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase  
CC activator (EC 3.1.4.12).  
CC -!- SUBUNIT: Saposin B is a homodimer.  
CC -!- SUBCELLULAR LOCATION: Lysosomal.  
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),



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Query Match 100.0%; Score 211; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.4e-18; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLKP 40
   |||||
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLKP 350

RESULT 2
ID SAP_BOVIN STANDARD; PRT; 525 AA.
AC P26779; Q9N2G4;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Proactivator polypeptide precursor [Contains: Saposin A (Protein A);
DE Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside
DE sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator);
DE Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase
DE activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
DE (Protein C) (Component C)].
GN PSAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN SEQUENCE FROM N.A., AND VARIANTS.
RC TISSUE=Mammary gland;
RA Azuma N., Yoshida K.;
RT "RT-PCR cloning of bovine prosaposin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 312-391.
RP TISSUE=Spleen;
RC MEDLINE=92207994; PubMed=1554743;
RA Sano A., Mizuno T., Kondoh K., Hinenio T., Ueno S.-I., Kakimoto Y.,
RA Morita N.;
RT "Saposin-C from bovine spleen; complete amino acid sequence and
RT relation between the structure and its biological activity.";
RL Biochim. Biophys. Acta 1120:75-80(1992).
CC -1- FUNCTION: THE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
CC BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
CC ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:
CC THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).
CC -1- FUNCTION: SAPO SIN A AND SAPO SIN C STIMULATE THE HYDROLYSIS OF
CC GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND
CC GALACTOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.46).
CC SAPO SIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
CC LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
CC THE SUBSTRATE.
CC -1- FUNCTION: SAPO SIN B STIMULATES THE HYDROLYSIS OF GALACTO-
CC CEREBROSIDE SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1
CC GANGLIOSIDES BY BETA-GALACTOSIDASE (EC 3.2.1.23) AND
CC GLOBOTRIOSYLCERAMIDE BY ALPHA-GALACTOSIDASE A (EC 3.2.1.22).
CC SAPO SIN B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE
CC SPHINGOLIPID HYDROLASES (BY SIMILARITY).
CC -1- FUNCTION: SAPO SIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE
CC ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).
CC -1- SUBUNIT: SAPO SIN B IS A HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- PTM: THIS PRECURSOR IS PROTEOLYTICALLY PROCESSED TO 4 SMALL
CC PEPTIDES, WHICH ARE SIMILAR TO EACH OTHER AND ARE SPHINGOLIPID
CC HYDROLASE ACTIVATOR PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 SAPO SIN A-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 SAPO SIN B-TYPE DOMAINS.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC EMBL; AB036791; BAA95677.1; -
DR PIR; S21770; S21770.
DR InterPro; IPR003119; SapA.
DR InterPro; IPR000004; SapB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapB; 4.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SAPB; 4.
KW Signal; Glycoprotein; Lysosome; Sphingolipid metabolism; Repeat.
FT SIGNAL 1 16
FT CHAIN 60 142
FT CHAIN 196 275
FT CHAIN 312 392
FT CHAIN 406 487
FT DOMAIN 21 54
FT DOMAIN 59 142
FT DOMAIN 194 276
FT DOMAIN 312 393
FT DOMAIN 406 487
FT DOMAIN 492 525
FT DISULFID 63 138
FT DISULFID 66 132
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FT DISULFID 231 242
FT DISULFID 316 389
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FT DISULFID 347 358
FT DISULFID 410 483
FT DISULFID 413 477
FT DISULFID 441 452
FT CARBOHYD 80 80
FT CARBOHYD 101 101
FT CARBOHYD 216 216
FT CARBOHYD 333 333
FT CARBOHYD 427 427
FT VARIANT 127 127
FT VARIANT 260 263
FT CONFLICT 317 317
FT CONFLICT 367 367
SQ SEQUENCE 525 AA; 58120 MW; 293AFC0FB9C4FA99 CRC64;

Query Match 82.9%; Score 175; DB 1; Length 525;
Best Local Similarity 77.5%; Pred. No. 1.6e-13;
Matches 31; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLKP 40
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 312 ADIYCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLKP 351

RESULT 3
SAP_CAVPO
ID SAP_CAVPO STANDARD; PRT; 81 AA.
AC P20097;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Saposin C (CO-beta-glucosidase) (Glucosylceramidase activator)
DE (Sphingolipid activator protein 2) (SAP-2).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
[1]
RN SEQUENCE.
RC TISSUE=Liver;
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RX MEDLINE-89066787; PubMed-3198642;
RA Sano A., Radin N.S., Johnson L.L., Tarr G.E.;
RT "The activator protein for glucosylceramide beta-glucosidase from
RT guinea pig liver. Improved isolation method and complete amino acid
RT sequence."
RL J. Biol. Chem. 263:19597-19601(1988).
CC -1- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
CC GLUCOSYLCEAMIDE BY BETA-GLUCOSYLCEAMIDASE (EC 3.2.1.45) AND
CC GALACTOSYLCEAMIDE BY BETA-GALACTOSYLCEAMIDASE (EC 3.2.1.46).
CC SAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
CC LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
CC THE SUBSTRATE.
CC -1- SIMILARITY: CONTAINS 1 SAPOSIN B-TYPE DOMAIN.
CC PIR; A32026; A32026.
DR HSP; P42210; IQDM.
DR InterPro: IPR000004; SApB.
DR ProDom; PD001732; SApB; 1.
DR SMART; SM00118; SApB; 1.
KW Glycoprotein; Sphingolipid metabolism.
FT DOMAIN 1 61 SAPOSIN-LIKE TYPE B.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .).
FT DISULFID 5 78 BY SIMILARITY.
FT DISULFID 8 72 BY SIMILARITY.
FT DISULFID 36 47 BY SIMILARITY.
SQ SEQUENCE 81 AA; 8852 MW; E564CE1F0A292596 CRC64;

Query Match 56.4%; Score 119; DB 1; Length 81;
Best Local Similarity 52.6%; Pred. No. 9.9e-08;
Matches 20; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 3 VYCEVFELVKEVTKLIDNNKTEKEITLDAFDKMSKLP 40
| : : : : : : : : : : : : : : : : : : : :
DB 3 VTCKACEYVVKVMELIDNNRTEKEITLDAFDKMSKLP 40

RESULT 4
SAP_CHICK STANDARD; PRT; 518 AA.
AC O13035;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Proactivator polypeptide precursor [Contains: Saposin A; Saposin B;
DE Saposin C; Saposin D].
GN PSAP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 194-203.
RC TISSUE=Brain, and Liver;
RX MEDLINE-98129745; PubMed-9461526;
RA Azuma N., Seo H.-C., Lie O., Fu Q., Gould R.M., Hiraiwa M., Burt D.W.,
RA Paton I.R., Morrice D.R., O'Brien J.S., Kishimoto Y.;
RT "Cloning, expression and map assignment of chicken prosaposin.";
RL Biochem. J. 330:321-327(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Altman N., Horowitz M.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
CC BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
CC ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS;
CC THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
CC GLUCOSYLCEAMIDE BY BETA-GLUCOSYLCEAMIDASE (EC 3.2.1.45) AND
CC GALACTOSYLCEAMIDE BY BETA-GALACTOSYLCEAMIDASE (EC 3.2.1.46).
CC SAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
CC LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
CC THE SUBSTRATE (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN B STIMULATES THE HYDROLYSIS OF GALACTO-

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```

CC CEREBROSIDE SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1
CC GANGLIOSIDES BY BETA-GALACTOSIDASE (EC 3.2.1.23) AND
CC GLOBOTRIAOSYLCEAMIDE BY ALPHA-GALACTOSIDASE A (EC 3.2.1.22).
CC SAPOSIN-B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE
CC SPHINGOLIPID HYDROLASES (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE
CC ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).
CC -1- SUBUNIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Lysosomal (BY SIMILARITY).
CC -1- PTM: THIS PRECURSOR IS PROTEOLYTICALLY PROCESSED TO 4 SMALL
CC PEPTIDES, WHICH ARE SIMILAR TO EACH OTHER AND ARE SPHINGOLIPID
CC HYDROLASE ACTIVATOR PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB003471; BAAL19914.1; -.
CC EMBL; AF108656; AAF05899.1; -.
CC InterPro: IPR003119; SApA.
CC InterPro: IPR000004; SApB.
CC Pfam; PF02199; SApA; 2.
CC ProDom; PD001732; SApB; 4.
CC SMART; SM00162; SApA; 2.
CC SMART; SM00118; SApB; 4.
CC Signal; Glycoprotein; Lysosome; Sphingolipid metabolism; Repeat;
KW GM2-gangliosidosis.
KW SIGNAL 1 17 POTENTIAL.
FT CHAIN 61 143 SAPOSIN A.
FT CHAIN 194 276 SAPOSIN B.
FT CHAIN 307 387 SAPOSIN C.
FT CHAIN 399 480 SAPOSIN D.
FT DOMAIN 22 55 SAPOSIN-LIKE TYPE A 1.
FT DOMAIN 60 143 SAPOSIN-LIKE TYPE B 1.
FT DOMAIN 193 277 SAPOSIN-LIKE TYPE B 2.
FT DOMAIN 307 388 SAPOSIN-LIKE TYPE B 3.
FT DOMAIN 399 480 SAPOSIN-LIKE TYPE B 4.
FT DOMAIN 485 518 SAPOSIN-LIKE TYPE A 2.
FT DISULFID 64 139 BY SIMILARITY.
FT DISULFID 67 133 BY SIMILARITY.
FT DISULFID 95 107 BY SIMILARITY.
FT DISULFID 197 273 BY SIMILARITY.
FT DISULFID 200 267 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 311 384 BY SIMILARITY.
FT DISULFID 314 378 BY SIMILARITY.
FT DISULFID 342 353 BY SIMILARITY.
FT DISULFID 403 476 BY SIMILARITY.
FT DISULFID 406 470 BY SIMILARITY.
FT DISULFID 434 445 BY SIMILARITY.
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 94 94 R -> T (IN REF. 2).
FT CONFLICT 486 486 E -> D (IN REF. 2).
SQ SEQUENCE 518 AA; 57601 MW; B803000E891C3963 CRC64;

Query Match 51.2%; Score 108; DB 1; Length 518;
Best Local Similarity 52.8%; Pred. No. 1.4e-05;
Matches 19; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 5 CEVCEFLVKEVTKLIDNNKTEKEITLDAFDKMSKLP 40
| : : : : : : : : : : : : : : : : : : : :
DB 311 CEICETWKEVTKLLESNKTEKEITVHEMEVVCYLLP 346

```



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```
CC EMBL; S36200; AAB22175.1; -
CC EMBL; S71616; AAB31059.1; -
CC EMBL; U27340; AAA92567.1; -
CC EMBL; U57999; AAB02695.1; -
CC MGD; MGI:97783; Psap.
CC InterPro; IPR003119; Sapa.
CC InterPro; IPR000004; SappB.
CC Pfam; PF02199; Sapa; 2.
CC ProDom; PD001732; Sapp; 4.
CC SMART; SM00162; Sapa; 2.
CC SMART; SM00118; Sapp; 4.
KW Sulfation; Signal; Glycoprotein; Repeat.
FT SIGNAL 1 16 BY SIMILARITY.
FT CHAIN 17 557 SULFATED GLYCOPROTEIN 1.
FT DOMAIN 21 54 SAPOSIN-LIKE TYPE A 1.
FT DOMAIN 59 142 SAPOSIN-LIKE TYPE B 1.
FT DOMAIN 193 277 SAPOSIN-LIKE TYPE B 2.
FT DOMAIN 313 394 SAPOSIN-LIKE TYPE B 3.
FT DOMAIN 438 519 SAPOSIN-LIKE TYPE B 4.
FT DOMAIN 524 557 SAPOSIN-LIKE TYPE A 2.
FT DISULFID 63 138 BY SIMILARITY.
FT DISULFID 66 132 BY SIMILARITY.
FT DISULFID 94 106 BY SIMILARITY.
FT DISULFID 197 273 BY SIMILARITY.
FT DISULFID 200 267 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 317 390 BY SIMILARITY.
FT DISULFID 320 384 BY SIMILARITY.
FT DISULFID 348 359 BY SIMILARITY.
FT DISULFID 442 515 BY SIMILARITY.
FT DISULFID 445 509 BY SIMILARITY.
FT DISULFID 473 484 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 83 83 Q -> E (IN REF. 2).
FT CONFLICT 158 158 I -> V (IN REF. 3).
FT CONFLICT 160 160 MISSING (IN REF. 2).
FT CONFLICT 171 172 MS -> SA (IN REF. 3).
FT CONFLICT 244 244 V -> L (IN REF. 2).
FT CONFLICT 254 254 M -> I (IN REF. 3).
FT CONFLICT 255 255 L -> W (IN REF. 2).
FT CONFLICT 260 262 MISSING (IN REF. 3).
FT CONFLICT 307 307 N -> D (IN REF. 2).
FT CONFLICT 322 322 F -> L (IN REF. 2).
FT CONFLICT 349 350 AL -> GV (IN REF. 1).
FT CONFLICT 367 367 G -> D (IN REF. 3).
FT CONFLICT 370 370 L -> Q (IN REF. 2).
FT CONFLICT 373 373 I -> D (IN REF. 3).
FT CONFLICT 391 391 R -> T (IN REF. 3).
FT CONFLICT 393 393 R -> L (IN REF. 3).
FT CONFLICT 406 406 A -> R (IN REF. 2 AND 3).
FT CONFLICT 430 430 P -> R (IN REF. 2).
FT CONFLICT 445 445 C -> F (IN REF. 3).
FT CONFLICT 448 448 L -> P (IN REF. 4).
FT SEQUENCE 557 AA; 61422 MW; 134593E20499E35E CRC64;
```

Query Match 40.3%; Score 85; DB 1; Length 557;  
Best Local Similarity 45.9%; Pred. No. 0.0081;  
Matches 17; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 4 YCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 40  
:||||: || : : : | :||| : ||| ||  
Db 441 FCEVCKLVLYLEHNLEKNSTKEELIAALEKGCSEFLP 477

RESULT 7

```
ASPR_ORYSA
ID ASPR_ORYSA STANDARD; PRT; 496 AA.
AC P42211.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aspartic proteinase precursor (EC 3.4.23.-).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Hashimoto H., Nishi R., Uchimiya H., Kato A.;
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
CC -| SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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```
CC -----
CC EMBL; D12777; BAA02242.1; -
CC BSSP; P42210; LODM.
CC MEROPS; A01.020; -
CC InterPro; IPR001461; AspproteaseA1.
CC InterPro; IPR001969; Aspprotease_site.
CC InterPro; IPR000004; SappB.
CC Pfam; PF00026; asp. 1.
CC PRINTS; PR00792; PEPSIN.
CC ProDom; PD001732; Sapp; 1.
CC SMART; SM00118; SAPP; 2.
CC PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Zymogen; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 59 POTENTIAL.
FT CHAIN 60 496 ASPARTIC PROTEINASE.
FT DOMAIN 310 408 SPECIFIC TO PLANT ASPARTIC PROTEINASES
FT ACT_SITE 95 95 BY SIMILARITY.
FT ACT_SITE 282 282 BY SIMILARITY.
FT DISULFID 108 114 BY SIMILARITY.
FT DISULFID 273 277 BY SIMILARITY.
FT DISULFID 415 452 BY SIMILARITY.
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 496 AA; 54104 MW; A273688E23B8F7E8 CRC64;
```



Query Match 37.9%; Score 80; DB 1; Length 496;  
Best Local Similarity 37.5%; Pred. No. 0.028;  
Matches 15; Conservative 9; Mismatches 16; Indels 0; Gaps 0;



QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 40  
||| ||| : : ||| : ||| : ||| : |||  
Db 366 SDAMCSVCEMVAVWIENQLRENKTELILNYANQLCERLP 405



RESULT 8  
ASPR_HORVU  
ID ASPR_HORVU STANDARD; PRT; 508 AA.  
AC P42210.  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE Phytapsin precursor (EC 3.4.23.40) (Aspartic proteinase).  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI_TaxID=4513;


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```
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable intron maturase (Maturase K).
GN MATK.
OS Torreyia californica (California nutmeg).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Torreya.
OX NCBI_TaxID=89482;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA MEDLINE=20179521; PubMed=10712841;
RX Cheng Y., Nicolson R.G., Tripp K., Chaw S.;
RT "Phylogeny of taxaceae and Cephalotaxaceae genera inferred from
RT chloroplast matk gene and nuclear rDNA ITS region.";
RL Mol. Phylogenet. Evol. 14:353-365(2000).
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS.
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
CC BY MITOCHONDRIAL INTRONS.
CC -----
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CC -----
CC EMBL: AB023998; BAA86047.1;
CC InterPro: IPR000442; Intron_maturase2.
CC InterPro: IPR002866; MatK_N.
CC Pfam: PF01348; Intron_maturase2; 1.
CC Pfam: PF01824; MatK_N; 1.
CC Chloroplast; mRNA processing.
SQ SEQUENCE 495 AA; 59260 MW; 939FB037285A36F8 CRC64;

Query Match 27.78; Score 58.5; DB 1; Length 495;
Best Local Similarity 35.94; Pred. No. 10;
Matches 14; Conservative 7; Mismatches 9; Indels 9; Gaps 1;

OY 10 FLVKE-----VTKLDNNKTEKILDAFDKMSKSL 39
DQ 372 FLAKEKCDISGHPISKLSWTSLTDDILDRFDRICINL 410

RESULT 13
Y890_METJA
ID Y890_METJA STANDARD; PRT; 137 AA.
AC Q8300;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein M30890.
GN M30890.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii.";
RA Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE UPF0148 FAMILY.
CC -----
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CC -----
CC EMBL: U67533; AAB98906.1;
CC TIGR: MJ0890;
CC InterPro: IPR005355; UPF0148.
CC Pfam: PF03680; UPF0148; 1.
CC Hypothetical protein; Complete proteome.
FT DOMAIN 131 135 LYS-RICH.
SQ SEQUENCE 137 AA; 15914 MW; BOEAC8A4245C0C8 CRC64;

Query Match 27.58; Score 58; DB 1; Length 137;
Best Local Similarity 32.44; Pred. No. 3;
Matches 12; Conservative 10; Mismatches 13; Indels 2; Gaps 1;

OY 3 VYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKSL 39
DQ 55 IYCPICEKLNKKT--IEKGENEKKEIRNEIERKASEI 89

RESULT 14
YF87_HELPJ
ID YF87_HELPJ STANDARD; PRT; 209 AA.
AC Q9ZJ25;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein JHP1493.
GN JHP1493.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human
RA gastric pathogen Helicobacter pylori.";
RA Nature 397:176-180(1999).
CC -!- SIMILARITY: BELONGS TO THE UPF0174 FAMILY.
CC -----
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CC -----
CC EMBL: AE001571; AAD07072.1;
CC InterPro: IPR005367; UPF0174.
CC Pfam: PF03667; UPF0174; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 209 AA; 22907 MW; C6EC950CDD424CAF CRC64;

Query Match 27.34; Score 57.5; DB 1; Length 209;
Best Local Similarity 26.24; Pred. No. 5.3;
```

	Matches	11;	Conservative	10;	Mismatches	16;	Indels	5;	Gaps	1;
QY	2	DVYCEVCEEL-----VKETKLDNNKTEKEILDADFDMCSK	38							
	::	: :: :	:	:: :	:	:: :	:			
Db	50	EILDCACDHLDIINVERSATSILEQNMLSKLLDKDSLERNMGR	91							

**RESULT 15**

```

ID YF87_HELPY STANDARD; PRRT; 209 AA.
O26106;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein HP1587.
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
NCBI_TaxID=210;
[1]
SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kervilave A.R., Klenk H.-P., Gill S., Dougherty B.A.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Kirschner E.F., Peterson S.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Hickey E.K.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathley L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
Venter J.C.;
"The complete genome sequence of the gastric pathogen Helicobacter
pylori";
Nature 388:539-547(1997).
[2]
CONCEPTUAL TRANSLATION.
Bairoch A.;
Unpublished observations (OCT-2001).
-1- SIMILARITY: BELONGS TO THE UPF0174 FAMILY.
-1- CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 160.
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-----
EMBL: AE000656; AAD08626.1; ALT_FRAME.
TIGR: HP1587.
InterPro: IPR005367; UPF0174.
Pfam: PF03667; UPF0174; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 209 AA; 23069 MW; F98D3FB8F362323 CRC64;

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```

Query Match      26.8%; Score 56.5; DB 1; Length 209;
Best Local Similarity 25.5%; Pred. NO. 7;
Matches 13; Conservative 11; Mismatches 14; Indels 13; Gaps 2;

QY      2 DVYECVCFEL-----VKETVKLIDNNKTEKEILDADKRM-----CSKL 39
      : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      50 EILDCADHLKLVNNEESATSLIEONMLSKLLKLDSEKMSRRRIEKLNCNEL 100

```

Search completed: June 2, 2003, 14:14:37  
Job time : 8.67949 secs





DE Naegleria A pore-forming peptide.

GN PRNP-A.

OS Naegleria fowleri.

OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.

OX NCBI\_TaxID=5763;

RN [1]

RP SEQUENCE FROM N.A.

RA Nickel R., Benkert C., Jacobs T., Marti T., Marciano-Cabral F.,

RA Leipe M.

RT "Pore-forming peptides of Naegleria fowleri."

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF154046; AK21658.1; -

DR InterPro: IPR000004; SApB.

DR ProDom: PD001732; SApB; 2.

DR SMART: SM00118; SApB; 3.

SQ SEQUENCE 307 AA; 33133 MW; 8503E4A755BC6DDF CRC64;

Query Match 44.5%; Score 94; DB 5; Length 307;

Best Local Similarity 35.9%; Pred. No. 0.0027;

Matches 14; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

YQ 2 DVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40

DB 117 DAECIECKFVIOQVEAFIESNHSQAEIQELNKLCSVP 155

| : : : : : | : : : : : | : : : : : | : : : : : |

| : : : : : | : : : : : | : : : : : | : : : : : |

| : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 3

Q8UV24

ID Q8UV24 PRELIMINARY; PRT; 520 AA.

AC Q8UV24;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Lysosomal cofactor/neurotrophic factor prosaposin.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Brachydanio; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Seo H.-C., Lie O., Fjose A., O'Brien J.S., Kishimoto Y.;

RT "Cloning, expression and promoter analysis of zebrafish prosaposin."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF276996; AAL54381.1; -

DR InterPro: IPR003119; SApB.

DR InterPro: IPR000004; SApB.

DR Pfam: PF02199; SApB; 2.

DR ProDom: PD001732; SApB; 3.

DR SMART: SM00162; SApB; 2.

DR SMART: SM00118; SApB; 4.

SQ SEQUENCE 520 AA; 57431 MW; F9E620F84BA41CB5 CRC64;

Query Match 43.6%; Score 92; DB 13; Length 520;

Best Local Similarity 38.9%; Pred. No. 0.0076;

Matches 14; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

YQ 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40

DB 312 CAICEYVMEIENMIQDTSEAEIVQAEKVCNLP 347

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RESULT 4

Q9DG82

ID Q9DG82 PRELIMINARY; PRT; 522 AA.

AC Q9DG82;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DE Prosaposin.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

GN Brachydanio; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Seo H.-C., Lie O., Fjose A., O'Brien J.S., Kishimoto Y.;

RT "Cloning, expression and promoter analysis of zebrafish prosaposin."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF276996; AAL54381.1; -

DR InterPro: IPR003119; SApB.

DR InterPro: IPR000004; SApB.

DR Pfam: PF02199; SApB; 2.

DR ProDom: PD001732; SApB; 3.

DR SMART: SM00162; SApB; 2.

DR SMART: SM00118; SApB; 4.

SQ SEQUENCE 520 AA; 57431 MW; F9E620F84BA41CB5 CRC64;

Query Match 43.6%; Score 92; DB 13; Length 520;

Best Local Similarity 38.9%; Pred. No. 0.0076;

Matches 14; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

YQ 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40

DB 312 CAICEYVMEIENMIQDTSEAEIVQAEKVCNLP 347

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DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE DE ASPARTIC PROTEINASE 2.
GN NAAp2.
OS Nepenthes alata (Winged pitcher plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Nepenthaceae; Nepenthes.
ON NCBI_TaxID=4376;
RN [1]
SEQUENCE FROM N.A.
RP An C., Fukusaki E., Kobayashi A.;
RT "Aspartic proteinases of carnivorous plant Nepenthes alata.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE
CC EUKARYOTIC ASPARTYL PROTEASES FAMILY.
DR EMBL; AB045892; BAE20970.1; -.
DR HSSP; P42210; IQDM.
DR MEROPS; A01.020; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR InterPro; IPR000004; SapB.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR ProDom; PD001732; SapB; 1.
DR SMART; SM00118; SAPB; 2.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Aspartyl protease; Hydrolase.
SQ SEQUENCE 514 AA; 55390 MW; F46C39A8090B5F55 CRC64;

Query Match 36.5%; Score 77; DB 10; Length 514;
Best Local Similarity 33.3%; Pred. No. 0.43;
Matches 13; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 2 DYVCEVCEFLVKEVTKLIDNNKTEKILDAFKMCKSLP 40
| | | | | : | | | | | : | | | | | : | | | | |
Db 385 DAMCTACEMAYVMQNLQRNRTTEQILNYVNELCNRLP 423

RESULT 9
Q9LGG3
ID Q9LGG3 PRELIMINARY; PRT; 495 AA.
AC Q9LGG3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ESTS AU031652(R0210).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoaceae; Oryza.
ON NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=CV. NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0469E05."
RL Submitted (JUN-2000) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE
CC EUKARYOTIC ASPARTYL PROTEASES FAMILY.
DR EMBL; AP002480; BAA96578.1; -.
DR HSSP; P42210; IQDM.
DR MEROPS; A01.020; -.
DR InterPro; IPR001589; Actbind_actnln.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR InterPro; IPR000004; SapB.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR ProDom; PD001732; SapB; 1.
DR SMART; SM00118; SAPB; 2.
DR PROSITE; PS00019; ACTININ.1; UNKNOWN.1.

```

0:



RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleab J.M.,  
RA Park S., Sequeira A., Sethi H., Snir E., Svirska R.R., Weinburg T.,  
RA Celniker S.E.;  
RT \*Full length Drosophila melanogaster cDNA sequence.\*;  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003775; AAF57097.1; -.  
DR EMBL; AF145647; AAD38622.1; -.  
DR FlyBase; FBgn0000416; Sap-r.  
DR InterPro; IPR003119; Sapa.  
DR InterPro; IPR000004; Sapa.  
DR Pfam; PF02199; SAPA; 1.  
DR ProDom; PD001732; Sapa; 6.  
DR SMART; SM00162; SAPA; 1.  
DR SMART; SM00118; SAPB; 7.  
SQ SEQUENCE 953 AA; 105962 MW; D6CFED3E9D1502A8 CRC64;

Query Match 34.6%; Score 73; DB 5; Length 953;  
Best Local Similarity 27.5%; Pred. No. 2.3;  
Matches 11; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEIILDADFDMCKSLP 40  
DB 68 TDSICTCKDMVTQARDQLKSNQTEELKEVFEKSLIP 107

Search completed: June 2, 2003, 14:17:17  
Job time : 28.6538 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:43 ; Search time 12.3077 Seconds  
(without alignments)  
95.624 Million cell updates/sec

Title: US-09-780-438c-1

Perfect score: 211

Sequence: 1 SDYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMGSKLP 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	80	1	US-08-100-247-3
2	211	100.0	80	1	US-08-483-146A-3
3	211	100.0	80	1	US-08-232-513A-4
4	211	100.0	80	1	US-08-484-594A-3
5	211	100.0	523	1	US-08-100-247-2
6	211	100.0	523	1	US-08-483-146A-2
7	211	100.0	523	1	US-08-232-513A-3
8	211	100.0	523	1	US-08-484-594A-2
9	111	52.6	22	1	US-08-100-247-1
10	111	52.6	22	1	US-08-483-146A-1
11	111	52.6	22	1	US-08-232-513A-1
12	111	52.6	22	1	US-08-484-594A-1
13	111	52.6	22	4	US-09-231-159-1
14	111	52.6	22	4	US-08-611-307-1
15	111	52.6	22	4	US-09-148-030-1
16	106	50.2	22	4	US-09-231-159-8
17	106	50.2	22	4	US-08-611-307-8
18	96	45.5	22	1	US-08-483-146A-9
19	96	45.5	22	1	US-08-232-513A-18
20	96	45.5	22	1	US-08-484-594A-9
21	96	45.5	22	4	US-09-231-159-7
22	96	45.5	22	4	US-08-611-307-7
23	83	39.3	18	1	US-08-100-247-5
24	83	39.3	18	1	US-08-483-146A-5
25	83	39.3	18	1	US-08-232-513A-6
26	83	39.3	18	1	US-08-484-594A-5
27	83	39.3	18	4	US-09-231-159-20

28	83	39.3	18	4	US-08-611-307-20	Sequence 20, Appl
29	83	39.3	18	4	US-09-148-030-2	Sequence 2, Appl
30	75	35.5	15	4	US-09-148-030-10	Sequence 10, Appl
31	75	35.5	22	1	US-08-483-146A-8	Sequence 8, Appl
32	75	35.5	22	1	US-08-232-513A-17	Sequence 17, Appl
33	75	35.5	22	1	US-08-484-594A-8	Sequence 8, Appl
34	75	35.5	22	4	US-09-231-159-6	Sequence 6, Appl
35	75	35.5	22	4	US-08-611-307-6	Sequence 9, Appl
36	64	30.3	14	4	US-09-231-159-9	Sequence 9, Appl
37	64	30.3	14	4	US-08-611-307-9	Sequence 9, Appl
38	63	29.9	14	4	US-09-231-159-10	Sequence 10, Appl
39	63	29.9	14	4	US-08-611-307-10	Sequence 10, Appl
40	63	29.9	15	4	US-09-148-030-9	Sequence 9, Appl
41	59	28.0	12	4	US-09-231-159-3	Sequence 3, Appl
42	59	28.0	12	4	US-08-611-307-3	Sequence 3, Appl
43	59	28.0	12	4	US-09-148-030-3	Sequence 3, Appl
44	57.5	27.3	388	4	US-09-134-001C-3820	Sequence 3820, Ap
45	55	26.1	78	2	US-08-732-228-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-100-247-3  
; Sequence 3, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; APPLICANT: KISHIMOTO, YASUO  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
; CITY: NEWPORT BEACH  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/100.247  
; FILING DATE: 19930730  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: O'BRIEN.002A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; IMMEDIATE SOURCE:  
; CLONE: SAPOSIN C  
; US-08-100-247-3

Query Match 100.0%; Score 211; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
|||||  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

RESULT 2  
US-08-483-146A-3  
; Sequence 3, Application US/08483146A  
; Patent No. 5696080  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED  
; TITLE OF INVENTION: THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Blvd. 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,146A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israel, Ned A  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: Internal  
US-08-483-146A-3

Query Match 100.0%; Score 211; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
|||||  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

RESULT 3  
US-08-232-513A-4  
; Sequence 4, Application US/08232513A  
; Patent No. 5700909  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides  
; TITLE OF INVENTION: as Therapeutic Agents  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,513A  
; FILING DATE: 21-APR-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/100,247  
; FILING DATE: 30-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1643  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1-80  
; OTHER INFORMATION: /label= saposin\_C  
US-08-232-513A-4

Query Match 100.0%; Score 211; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
|||||  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

RESULT 4  
US-08-484-594A-3  
; Sequence 3, Application US/08484594A  
; Patent No. 5714459  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES  
; TITLE OF INVENTION: DERIVED THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,594A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,247



;; FILING DATE: 30-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Israelsen, Ned A  
;; REGISTRATION NUMBER: 29,655  
;; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
;; TELEPHONE: 619-235-8550  
;; TELEFAX: 619-235-0176  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 80 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: internal  
;; US-08-484-594A-3

Query Match 100.0%; Score 211; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 40  
|||||  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 40

RESULT 5  
US-08-100-247-2  
; Sequence 2, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; APPLICANT: KISHIMOTO, YASUO  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
; CITY: NEWPORT BEACH  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/100,247  
; FILING DATE: 19930730  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: OBRIEN.002A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 523 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; IMMEDIATE SOURCE:  
; CLONE: PROSAPOSIN  
US-08-100-247-2

Query Match 100.0%; Score 211; DB 1; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 40  
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Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 349

RESULT 6  
US-08-483-146A-2  
; Sequence 2, Application US/08483146A  
; Patent No. 5696080  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED  
; FROM THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Blvd. 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/08/483,146A  
; APPLICATION NUMBER: 29,655  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 523 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
US-08-483-146A-2

Query Match 100.0%; Score 211; DB 1; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 40  
|||||  
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKSLP 349

RESULT 7  
US-08-232-513A-3  
; Sequence 3, Application US/08232513A  
; Patent No. 5700909  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
US-08-100-247-2

;  
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides  
; TITLE OF INVENTION: as Therapeutic Agents  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,513A  
; FILING DATE: 21-APR-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/100,247  
; FILING DATE: 30-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1643  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 523 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..523  
; OTHER INFORMATION: /label= Hum\_prosaposin  
US-08-232-513A-3  
  
Query Match 100.0%; Score 211; DB 1; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMGSKLP 40  
|||||  
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMGSKLP 349  
  
RESULT 8  
US-08-484-594A-2  
; Sequence 2, Application US/08484594A  
; Patent No. 5714459  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:

;  
; APPLICATION NUMBER: US/08/484,594A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,247  
; FILING DATE: 30-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israel, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 523 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
US-08-484-594A-2  
  
Query Match 100.0%; Score 211; DB 1; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMGSKLP 40  
|||||  
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMGSKLP 349  
  
RESULT 9  
US-08-100-247-1  
; Sequence 1, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; APPLICANT: KISHIMOTO, YASUO  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
; CITY: NEWPORT BEACH  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/100,247  
; FILING DATE: 19930730  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israel, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: O'BRIEN.002A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; CLONE: 22-MER FRAGMENT
US-08-100-247-1
Query Match 52.6%; Score 111; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

RESULT 10
US-08-483-146A-1
; Sequence 1, Application US/08483146A
; Patent No. 5696080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPIC PEPTIDES DERIVED
; FROM THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-483-146A-1
Query Match 52.6%; Score 111; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

RESULT 11
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US-08-232-513A-1
; Sequence 1, Application US/08232513A
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /label= SapC
US-08-232-513A-1
Query Match 52.6%; Score 111; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

RESULT 12
US-08-484-594A-1
; Sequence 1, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/484,594A  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/100,247  
;; FILING DATE: 30-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Israelsen, Ned A  
;; REGISTRATION NUMBER: 29,655  
;; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-235-8550  
;; TELEFAX: 619-235-0176  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
US-08-484-594A-1

Query Match 52.6%; Score 111; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

RESULT 13  
US-09-231-159-1  
; Sequence 1, Application US/09231159  
; Patent No. 6268347  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaiposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE:  
; CLASSIFICATION:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE: 05-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-09-231-159-1  
Query Match 52.6%; Score 111; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

RESULT 14  
US-08-611-307-1  
; Sequence 1, Application US/08611307  
; Patent No. 6271196  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaiposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611,307  
; FILING DATE: 05-MAR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-611-307-1

Query Match 52.6%; Score 111; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
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Db 1 CEFLVKEVTKLIDNNKTEKIL 22

RESULT 15  
US-09-148-030-1  
; Sequence 1, Application US/09148030C  
; Patent No. 6458357  
; GENERAL INFORMATION:  
; APPLICANT: White, Michael T.  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Wright, David E.  
; TITLE OF INVENTION: RETRO-INVERSO NEUTROTROPHIC AND ANALGESIC

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; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: MYELOS.004CPI
; CURRENT APPLICATION NUMBER: US/09/148,030C
; CURRENT FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 08/926,015
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-148-030-1

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Query Match      52.6%; Score 111; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 CEFVLVKEVTKLIDNNKTEKEIL 29
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Db      1 CEFVLVKEVTKLIDNNKTEKEIL 22

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Search completed: June 2, 2003, 14:18:23
Job time : 12.8077 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:18 ; Search time 15.8974 Seconds  
(without alignments)  
254.692 Million cell updates/sec

Title: US-09-780-438c-1

Perfect score: 211

Sequence: 1 SDVCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pdb.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pdb.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pdb.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pdb.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pdb.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	211	100.0	40	9	US-09-780-438A-1
2	211	100.0	80	10	US-09-767-007A-3
3	211	100.0	80	10	US-09-753-126-3
4	211	100.0	209	9	US-10-043-487-340
5	211	100.0	523	10	US-09-767-007A-2
6	211	100.0	524	9	US-09-870-759-60
7	211	100.0	527	9	US-09-870-759-61
8	211	100.0	527	9	US-10-060-036-73
9	211	100.0	592	10	US-09-753-126-4
10	201	95.3	38	9	US-09-780-438A-2
11	111	52.6	22	10	US-09-767-007A-1
12	111	52.6	22	10	US-09-957-143-1
13	96	45.5	22	10	US-09-767-007A-9
14	83	39.3	18	10	US-09-767-007A-5
15	83	39.3	18	10	US-09-957-143-2
16	75	35.5	15	9	US-10-293-819-2
17	75	35.5	15	10	US-09-802-617-2
18	75	35.5	22	10	US-09-767-007A-8
19	59	28.0	12	9	US-10-293-819-1

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Sequence 3, Appli  
Sequence 8, Appli  
Sequence 36091, A  
Sequence 15, Appli  
Sequence 8, Appli  
Sequence 3, Appli  
Sequence 338, App  
Sequence 2, Appli  
Sequence 367, App  
Sequence 1417, Ap  
Sequence 984, App  
Sequence 2, Appli  
Sequence 214, App  
Sequence 172, App  
Sequence 246, App  
Sequence 388, App  
Sequence 1335, A  
Sequence 6, Appli  
Sequence 9, Appli  
Sequence 5370, Ap  
Sequence 12552, A  
Sequence 12898, A  
Sequence 206, App  
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289 10 US-09-764-864-984  
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751 9 US-10-060-036-172  
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187 9 US-09-986-480-368  
418 10 US-09-815-242-13335  
22 10 US-09-767-007A-6  
179 9 US-10-135-807-9  
843 10 US-09-815-242-5370  
843 10 US-09-815-242-12552  
843 10 US-09-815-242-12898  
62 10 US-09-205-658-206  
100 9 US-09-820-473-4  
100 10 US-09-820-408-4

#### ALIGNMENTS

##### RESULT 1

US-09-780-438A-1  
; Sequence 1, Application US/09780438A  
; Publication No. US20030095999A1

; GENERAL INFORMATION:  
; APPLICANT: Cincinnati Childrens Hospital Research Foundation

; TITLE OF INVENTION: Fusogenic Properties of Saposin C and Related Proteins and Po

; FILE REFERENCE: 10872/0474352  
; CURRENT APPLICATION NUMBER: US/09/780,438A

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,754

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 1

; TYPE: PRT

; LENGTH: 40

; ORGANISM: Homo sapiens

US-09-780-438A-1

Query Match 100.0%; Score 211; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 7.8e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40

DB 1 SDVCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40

##### RESULT 2

US-09-767-007A-3  
; Sequence 3, Application US/09767007A  
; Patent No. US20020077275A1

; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien

; APPLICANT: Yasuo Kishimoto

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING

; FILE REFERENCE: MYELOS.DCIC1  
; CURRENT APPLICATION NUMBER: US/09/767,007A

; CURRENT FILING DATE: 2001-01-22

; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows version 4.0  
; SEQ ID NO 3  
; LENGTH: 80  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-3

Query Match 100.0%; Score 211; DB 10; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.7e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
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Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

## RESULT 3

US-09-753-126-3  
; Sequence 3, Application US/09753126  
; Patent No. US20020127219A1  
; GENERAL INFORMATION:  
; APPLICANT: ORKELS, JENS SIGURD  
; APPLICANT: JENSEN, ANNE DAM  
; APPLICANT: HALKIER, TORBEN  
; APPLICANT: JENSEN, RIKKE BOLDING  
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME  
; FILE REFERENCE: 31-000600US  
; CURRENT APPLICATION NUMBER: US/09/753,126  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: PA 1999 01891  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: 60/174,652  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: PA 200 00865  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/210,984  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: 60/211,124  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: PA 2000 01027  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/217,497  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 80  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-753-126-3

Query Match 100.0%; Score 211; DB 10; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.7e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
|||||  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

## RESULT 4

US-10-043-487-340  
; Sequence 340, Application US/10043487  
; Publication No. US20030055220A1  
; GENERAL INFORMATION:  
; APPLICANT: HYBRIGENICS  
; APPLICANT: Pierre, LEGRAIN

; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep  
; FILE REFERENCE: B4778A  
; CURRENT APPLICATION NUMBER: US/10/043,487  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/261,130  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 561  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 340  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Shigella Flexneri  
US-10-043-487-340

Query Match 100.0%; Score 211; DB 9; Length 209;  
Best Local Similarity 100.0%; Pred. No. 5e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
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Db 161 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 200

## RESULT 5

US-09-767-007A-2  
; Sequence 2, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; FILE REFERENCE: MYELOS 2DG1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 523  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-767-007A-2

Query Match 100.0%; Score 211; DB 10; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40  
|||||  
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 349

## RESULT 6

US-09-870-759-60  
; Sequence 60, Application US/09870759  
; Patent No. US20020177551A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 60  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: Homo sapiens



## US-09-870-759-60

Query Match 100.0%; Score 211; DB 9; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40  
|||||  
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 350

## RESULT 7

US-09-870-759-61  
; Sequence 61, Application US/09870759  
; Patent No. US20020177551A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 61  
; LENGTH: 527  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-870-759-61

Query Match 100.0%; Score 211; DB 9; Length 527;  
Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40  
|||||  
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 353

## RESULT 8

US-10-060-036-73  
; Sequence 73, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yuqiu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 527  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-060-036-73

Query Match 100.0%; Score 211; DB 9; Length 527;  
Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40  
|||||  
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 353

## RESULT 9

US-09-753-126-4  
; Sequence 4, Application US/09753126  
; Patent No. US20020127219A1  
; GENERAL INFORMATION:  
; APPLICANT: OKKELS, JENS SIGURD  
; APPLICANT: JENSEN, ANNE DAM  
; APPLICANT: HALKIER, TORBEN  
; APPLICANT: JENSEN, RIKKE BOLDING  
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME  
; TITLE OF INVENTION: ACTIVATORS  
; FILE REFERENCE: 31-00060005  
; CURRENT APPLICATION NUMBER: US/09/753,126  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: PA 1999 01891  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: 60/174,652  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: PA 200 00865  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/210,984  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: 60/211,124  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: PA 2000 01027  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/217,497  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
; OTHER INFORMATION: SapC-linker-GCB polypeptide  
US-09-753-126-4

Query Match 100.0%; Score 211; DB 10; Length 592;  
Best Local Similarity 100.0%; Pred. No. 1.6e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40  
|||||  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLP 40

## RESULT 10

US-09-780-438A-2  
; Sequence 2, Application US/09780438A  
; Publication No. US2003009599A1  
; GENERAL INFORMATION:  
; APPLICANT: Cincinnati Childrens Hospital Research Foundation  
; TITLE OF INVENTION: Fusogenic Properties of Saposin C and Related Proteins and Po  
; FILE REFERENCE: 10872/0474352  
; CURRENT APPLICATION NUMBER: US/09/780,438A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,754  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-780-438A-2

Query Match 95.3%; Score 201; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.5e-19;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLP 40  
|||||  
Db 1 YCEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSLP 38

## RESULT 11

US-09-767-007A-1  
; Sequence 1, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; FILE OF INVENTION: SAPOSIN C AND NEUTROTROPIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-1

Query Match 52.6%; Score 111; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.5e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
|||||  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

## RESULT 12

US-09-957-143-1  
; Sequence 1, Application US/09957143  
; Patent No. US20020128193A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: David E. Wright  
; TITLE OF INVENTION: RETRO-INVERSO PROSAPOSIN-DERIVED  
; FILE OF INVENTION: PEPTIDES AND USE THEREOF  
; FILE REFERENCE: MYELOS.018C1  
; CURRENT APPLICATION NUMBER: US/09/957,143  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: PCT/US00/08550  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/126,991  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-957-143-1

Query Match 52.6%; Score 111; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.5e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
|||||  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

## RESULT 13

US-09-767-007A-9  
; Sequence 9, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; FILE OF INVENTION: SAPOSIN C AND NEUTROTROPIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-9

Query Match 45.5%; Score 96; DB 10; Length 22;  
Best Local Similarity 81.8%; Pred. No. 4.1e-06;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
|||||  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

## RESULT 14

US-09-767-007A-5  
; Sequence 5, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; FILE OF INVENTION: SAPOSIN C AND NEUTROTROPIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-5

Query Match 39.3%; Score 83; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KEVTKLIDNNKTEKIL 29  
|||||  
Db 2 KEVTKLIDNNKTEKIL 18

## RESULT 15

US-09-957-143-2  
; Sequence 2, Application US/09957143  
; Patent No. US20020128193A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: David E. Wright

```
; TITLE OF INVENTION: RETRO-INVERSO PROSAPOSIN-DERIVED
; TITLE OF INVENTION: PEPTIDES AND USE THEREOF
; FILE REFERENCE: MYELOS.018C1
; CURRENT APPLICATION NUMBER: US/09/957,143
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: PCT/US00/08550
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/126,991
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-957-143-2
```

```
Query Match 39.3%; Score 83; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 13 KEVTKLIDNNKTEKIL 29
| | | | | | | | | | | | | | | |
Db 2 KEVTKLIDNNKTEKIL 18
```

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Search completed: June 2, 2003, 14:17:53
Job time : 16.8974 secs
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Best Local Similarity 55.9%; Pred. No. 4.6e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXNDNKKEXKXDXDXKXCKX 36  
DB 315 CEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSK 348

## RESULT 6

AAW85652  
ID AAW85652 standard; Protein; 524 AA.

XX AC AAW85652;

XX DT 19-JUL-1999 (first entry)

XX DE Human prosaposin N-terminal peptide.

XX KW Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
XX KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
XX KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
XX KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
XX KW inflammation; rheumatoid arthritis; Crohn's disease;  
XX KW irritable bowel syndrome; asthma; cardiac infarction;  
XX KW congestive heart failure; multiple sclerosis;  
XX KW acute disseminated inflammatory leukoencephalitis;  
XX KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
XX KW Parkinson's disease; amyotrophic lateral sclerosis;  
XX KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
XX KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy; disease;  
XX KW inflammatory neurodegenerative disease; toxin-induced liver disease.

XX OS Homo sapiens.

XX PN WO9912559-A1.

XX PD 18-MAR-1999.

XX PF 09-SEP-1998; 98WO-US19216.

XX PR 04-JUN-1998; 98US-0088129.

XX PR 09-SEP-1997; 97US-0058352.

XX PA (REGC ) UNIV CALIFORNIA.

XX XX O'Brien JS;

XX XX WPI; 1999-229139/19.

XX XX N-PSDB; AAX08488.

XX PT Use of prosaposin receptor agonist

XX PS Claim 7; Figure 2; 90pp; English.

XX CC Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
XX CC to generate saposins A, B, C and D, all of which are similar to each  
XX CC other and have a similar placement of six cysteines, a glycosylation  
XX CC site and conserved proline residues. Prosaposin, saposin C and  
XX CC prosaposin derived peptides (prosaptides), have therapeutic  
XX CC applications in promoting recovery after toxic, traumatic, myocardial  
XX CC ischaemic, degenerative and inherited lesions to the peripheral and  
XX CC central nervous system. Prosaposin receptor agonists (PRAs)  
XX CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
XX CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
XX CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
XX CC members which inhibit caspases, thereby inhibiting apoptosis. An  
XX CC additional mechanism whereby PRAs inhibit apoptosis is by blocking  
XX CC activation of JNK, a proapoptotic signaling component. Within  
XX CC several minutes after binding to the receptor, PRAs block JNK  
XX CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
XX CC activation of JNK by TNF alpha is another well known mechanism for  
XX CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
XX CC apoptosis. The method can be used for inhibiting apoptosis which is

CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. This 524 N-terminal peptide of prosaposin also acts  
CC as a prosaposin receptor agonist.

XX SQ Sequence 524 AA;

Query Match 77.1%; Score 101; DB 20; Length 524;  
Best Local Similarity 55.9%; Pred. No. 4.6e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXNDNKKEXKXDXDXKXCKX 36  
DB 315 CEVCEFLVKEVTKLIDNNKTEKILDAFDMCKSK 348

## RESULT 7

AAV58716

ID AAV58716 standard; Protein; 524 AA.

XX AC AAV58716;

XX DT 25-APR-2000 (first entry)

XX DE Human prosaposin.

XX KW Prosaposin; saponin B; antiangiogenic; angiogenesis inhibitor;  
XX KW antitumour; antiproliferative; antimigratory; Kaposi's sarcoma;  
XX KW tumour; human; therapy.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Protein /note= "mature saposin B"

XX FT Peptide /note= "specifically claimed antiangiogenic peptide"

XX FT Peptide /note= "specifically claimed antiangiogenic peptide"

XX FT Peptide /note= "specifically claimed antiangiogenic peptide"

XX FT Peptide /note= "specifically claimed antiangiogenic peptide"

XX FT Peptide /note= "specifically claimed antiangiogenic peptide"

XX FT Peptide /note= "specifically claimed antiangiogenic peptide"

XX FT Peptide /note= "specifically claimed antiangiogenic peptide"

XX PN WO200002902-A1.

XX PD 20-JAN-2000.

XX PF 12-JUL-1999; 99WO-US15772.

XX PR 13-JUL-1998; 98US-0092647.

XX XX (GILL/) GILL P S.

XX XX GILL PS;

XX XX WPI; 2000-171128/15.

XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and  
XX PT tumor growth -

XX PS Disclosure; Page 18; 78pp; English.

XX CC The present sequence is that of human prosaposin, a precursor of  
XX CC saposin B. The invention is based on the discovery that saposin B,  
XX CC previously known to be involved in the hydrolysis of sphingolipids,



CC has potent antiangiogenic and antitumour activity, and also has  
 CC antiproliferative and antimigratory activity against endothelial  
 CC cells. This activity is conserved in cryptic polypeptides as small  
 CC as 5 amino acids (see AA58684-715), which can be synthetically  
 CC prepared and used in vitro or in vivo for the treatment of  
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma  
 CC (claimed). The polypeptides can also be used in conjunction with  
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for  
 CC treatment of cancer, angiodioma, neovascular glaucoma,  
 CC arteriovenous malformation, nonunion fracture, arthritis and other  
 CC connective tissue disorders, Osler-Weber syndrome, atherosclerotic  
 CC plaque, psoriasis, corneal graft neovascularization, pyogenic  
 CC granuloma, retrolental fibroplasia, diabetic retinopathy,  
 CC scleroderma, haemangioma, trachoma, vascular adhesions and  
 CC hypertrophic scars.

XX SQ Sequence 524 AA;

Query Match 77.1%; Score 101; DB 21; Length 524;  
 Best Local Similarity 55.9%; Pred. No. 4.6e-09;  
 Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXNDNNKXKEXKXDXKXKXK 36  
 DB 315 CEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCK 348

RESULT 8

AA331915

ID AAB31915 standard; Protein: 527 AA.

XX AC AAB31915;

XX DT 15-MAY-2001 (first entry)

XX DE Amino acid sequence of a human protein.

XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;  
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;  
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;  
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX Homo sapiens.

XX WO200105422-A2.

XX 25-JAN-2001.

XX PF 17-JUL-2000; 2000WO-FR02057.

XX PR 15-JUL-1999; 99FR-0009372.

XX PA (INMR ) BIOMERIEUX STELHYS.

XX PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;  
 XX WPI; 2001-159475/16.

XX PT Detecting, preventing and treating degenerative, neurological and  
 PT autoimmune diseases, particularly multiple sclerosis, using specified  
 PT polypeptides or related nucleic acid or ligand -

XX Claim 1; Page 172-173; 209pp; French.

XX The present sequence represents a human protein, which is used in the  
 CC method of the invention. The specification describes a method which uses  
 CC at least one polypeptide or polynucleotide sequence belonging to the  
 CC perlecan, precursor of the retinol-binding plasma protein, precursor of  
 CC the ganglioside GM2 activator, calgranulin B or saposin B protein  
 CC families. The method is used for detecting, preventing or treating a  
 CC degenerative, neurological and/or auto-immune disease. The  
 CC polynucleotides and polypeptides are used for diagnosis, prognosis,

CC prevention and treatment of multiple sclerosis (in its various forms  
 CC and phases). They may also be useful in cases of e.g. Alzheimer's and  
 CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid  
 CC polyarthritis and lupus erythematosus, including use as vaccines and  
 CC in gene therapy (expression of sense or antisense sequences). They can  
 CC also be used to assess efficacy of potential therapeutic agents,  
 CC particularly compounds that reduce or inhibit toxicity towards glial  
 CC cells.

XX SQ Sequence 527 AA;

Query Match 77.1%; Score 101; DB 22; Length 527;  
 Best Local Similarity 55.9%; Pred. No. 4.6e-09;  
 Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXNDNNKXKEXKXDXKXKXK 36  
 DB 318 CEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCK 351

RESULT 9

AAU05698

ID AAU05698 standard; Protein: 592 AA.

XX AC AAU05698;

XX DT 24-OCT-2001 (first entry)

XX DE Human glucocerebrosidase, GCB-Saponin C, SapC, fusion protein.

XX Human; glucocerebrosidase; GCB; lysosomal storage disease;  
 KW Gaucher's disease; Fabry's disease; Farber's disease;  
 KW G.M.I gangliosidosis; Tay-Sach's disease; Niemann-Pick disease;  
 KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;  
 KW Schele syndrome; fusion protein; Saponin C; SapC.

XX OS Homo sapiens.

XX OS Synthetic.

XX Key Location/Qualifiers

XX Protein 1..80

XX Peptide /label= SapC

XX FT 81..95

XX FT /label= Linker\_peptide

XX FT 96..592

XX FT /label= GCB

XX FT Modified-site 114

XX FT /note= "N-glycosylated"

XX FT Modified-site 154

XX FT /note= "N-glycosylated"

XX FT Modified-site 241

XX FT /note= "N-glycosylated"

XX FT Modified-site 365

XX FT /note= "N-glycosylated"

XX WO200149830-A2.

XX 12-JUL-2001.

XX PF 29-DEC-2000; 2000WO-DK00743.

XX PR 30-DEC-1999; 99DK-0001891.

XX PR 02-JUN-2000; 2000DK-0000865.

XX PR -02-JUN-2000; 2000DK-0000866.

XX PR 30-JUN-2000; 2000DK-0001027.

XX PA (MAXY-) MAXYGEN APS.

XX PI Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;  
 XX WPI; 2001-465259/50.

XX DR Improved lysosomal enzymes and lysosomal enzyme activators useful for

PT treating Gaucher's disease -

PS Example 5; Page 96-97; 97pp; English.

XX The sequence is a fusion protein of human lysosomal enzyme  
CC glucocerebrosidase, GCB and its co-factor, Saponin C, SapC.  
CC GCB is the enzyme involved in Gaucher's disease, a lysosomal  
CC storage disease. The invention relates to introducing new glycosylation  
CC sites into lysosomal enzymes/activators like GCB to improve their  
CC bioactivity. The novel polypeptides are used for the prevention and  
CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,  
CC G<sub>M</sub>-1 gangliosidosis, Tay-Sachs's disease, Niemann-Pick disease, Shindler  
CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie  
CC syndromes.

XX Sequence 592 AA;

SQ Query Match 77.1%; Score 101; DB 22; Length 592;

Best Local Similarity 55.9%; Pred. No. 5.2e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKXKXNDNNKXEXXDXDKXCXK 36

DB 5 CEVCEFLVKEVTKLIDNNKTEKEILDFAFKMCKS 38

RESULT 10

AAB67289

ID AAB67289 standard; Peptide; 25 AA.

XX AAB67289;

XX 20-APR-2001 (first entry)

XX Human saposin C.

XX Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.

XX Homo sapiens.

XX EP1072609-A2.

XX 31-JAN-2001.

XX 30-JUN-2000; 2000EP-0305504.

XX 30-JUN-1999; 99JP-0185155.

XX (SAKA/) SAKANAKA M.

XX (TANA/) TANAKA J.

XX (SATO/) SATO K.

XX Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;

XX WPI; 2001-204263/21.

XX Use of prosaposin-related peptides or derivatives as cytoprotective  
PT agents, for suppressing apoptosis or apoptosis-like cell death -

XX Disclosure; Page 12; 41pp; English.

XX The present invention relates to use of a prosaposin-related peptide  
CC or derivative, in the production of a medicament for use in  
CC preventing or delaying cell death, or in promoting the expression  
CC of cell death supporting gene product Bcl-XL. The invention is  
CC useful for preventing the death of cells e.g. brain cells,  
CC neurons and cardiac muscle cells, in vitro or ex vivo.

XX Sequence. 25 AA;

SQ Query Match 49.6%; Score 65; DB 22; Length 25;

Best Local Similarity 56.5%; Pred. No. 0.00029;  
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 CEXXXKXKXNDNNKXEXXDX 28

DB 1 CEFLVKEVTKLIDNNKTEKEILD 23

RESULT 11

AAY82281

ID AAY82281 standard; peptide; 21 AA.

XX AAY82281;

XX 16-JUN-2000 (first entry)

XX Human saposin C 22-mer peptide SEQ ID NO:1.

XX Cyclic; prosaposin; neurotrophic; analgesic; neural growth; cell death;  
KW myelination; neurodegenerative disorder; neuropathic pain; vasotropic;  
KW saposin C; neuroprotective; vulnery; analgesic; antiparkinsonian;  
KW ophthalmological; demyelination; multiple sclerosis; ischaemic injury;  
KW traumatic injury; Parkinson's disease; retinal neuropathy;  
KW ocular neurodegeneration.

XX Homo sapiens.

XX WO200012553-A1.

XX 09-MAR-2000.

XX 20-AUG-1999; 99WO-US19378.

XX 28-AUG-1998; 98US-0098359.

XX (MYEL-) MYELOS CORP.

XX Wright DE, O'Brien JS;

XX WPI; 2000-256591/22.

XX New peptide derived from saposin C, useful to treat demyelination,  
PT neural degeneration and neurological pain, is circular and thus  
PT resistant to proteolytic degradation -

XX Disclosure; Page 2; 30pp; English.

XX The present invention describes a cyclic peptide of about 11-25 amino  
CC acids containing an analogue of the 11-mer active region of saposin C.  
CC The cyclic peptide has neuroprotective, vasotropic, vulnery,  
CC analgesic, antiparkinsonian and ophthalmological activities. It  
CC stimulates choline acetyltransferase activity. The peptide is used to  
CC induce myelination or inhibit demyelination in a mammal, especially a  
CC human, where demyelination is due to multiple sclerosis, ischaemic  
CC injury or traumatic injury, to inhibit neural degeneration or promote  
CC neurite outgrowth in neural tissue and treat neuropathic pain. The  
CC peptide may also be useful to treat Parkinson's disease, retinal  
CC neuropathy, and ocular neurodegeneration leading to vision loss in the  
CC elderly. The peptide can be used in research to study the effects of  
CC neurotrophic factors and myelin facilitating materials, and as  
CC components of cell growth media for facilitating and maintaining neural  
CC cells in vitro. The invention provides circular prosaposin  
CC peptidomimetics which are more resistant to proteolytic degradation and  
CC better able to cross the blood brain barrier than prior art linear  
CC peptides. The present sequence represents a human saposin C 22-mer  
CC peptide given in the disclosure of the present invention.

XX Sequence 21 AA;

SQ Query Match 46.6%; Score 61; DB 21; Length 21;

Best Local Similarity 60.0%; Pred. No. 0.0011;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKXKXNDNNKXEXKE 25

DB 1 CEXXXKXKXNDNNKXEXKE 25

Db 1 CEFLVKEVTKLIDNNKTEKE 20

# RESULT 12

AAR70773  
ID AAR70773 standard; peptide; 22 AA.

XX AC AAR70773;

XX XX 30-AUG-1995 (first entry)  
XX XX Saposin-C neurotrophic peptide.

DE XX Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW KW adrenal leukodystrophy.

XX OS Homo sapiens.

XX PN WO9503821-A.

XX PD 09-FEB-1995.

XX PE 28-JUL-1994; 94WO-US08453.

XX PR 30-JUL-1993; 93US-0100247.

XX PR 21-APR-1994; 94US-0232513.

XX PA (OBRI/) OBRIEN J S.

XX PI Kishimoto Y, Obrien JS;

XX DR WPI; 1995-082029/11.

XX XX Stimulating neural cell out-growth and myelination - with  
PT pro:saposin, saposin C or new neurotrophic peptide(s) from  
PT cytokine(s), for treating nervous system diseases  
XX XX Disclosure; Page 30; 50pp; English.

XX XX The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neurotrophic cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosapoin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.

XX SQ Sequence 22 AA;

Query Match 46.6%; Score 61; DB 16; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXKXXDNNKXEKE 25  
II II I III III  
Db 1 CEFLVKEVTKLIDNNKTEKE 20

# RESULT 13

AAW30013  
ID AAW30013 standard; peptide; 22 AA.

XX AC AAW30013;

XX XX 14-APR-1998 (first entry)  
XX XX Prosapoin-derived peptide 22-mer.

DE XX Human; prosapoin; neural disorder; demyelination disorder;  
KW KW neural cell death; inhibition; myelination; neurite outgrowth;

KW neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy;  
KW polynuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus.

OS Homo sapiens.

XX PN WO9732895-A1.

XX PD 12-SEP-1997.

XX XX 05-MAR-1997; 97WO-US04143.

XX PR 05-MAR-1996; 96US-0611307.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI O'Brien JS;

XX DR WPI; 1997-470538/43.

XX XX Prosapoin-derived peptide - useful for therapy of neural or  
PT demyelination disorders in neural tissue  
XX XX Claim 9; Page 52; 69pp; English.

XX CC The present sequence represents a prosapoin-derived peptide. A method  
CC has been developed of alleviating or preventing neuropathic pain in a  
CC subject, comprising administering an effective amount of an active  
CC fragment of prosapoin to the subject. The prosapoin-derived peptide  
CC is useful for therapy of neural or demyelination disorders in neural  
CC tissue. It can be used to stimulate neurite outgrowth, inhibit neural  
CC cell death, promote myelination or inhibit demyelination. The method  
CC is used to alleviate neuropathic pain resulting from a peripheral nerve  
CC disorder, such as neuroma, nerve compression, crush or stretch and  
CC incomplete nerve transection, mononeuropathy or polynuropathy.  
CC Alternatively the neuropathic pain results from a disorder of the  
CC dorsal root ganglia, spinal cord, brainstem, thalamus or cortex.

XX SQ Sequence 22 AA;

Query Match 46.6%; Score 61; DB 18; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXKXXDNNKXEKE 25  
II II I III III  
Db 1 CEFLVKEVTKLIDNNKTEKE 20

# RESULT 14

AAW66127  
ID AAW66127 standard; peptide; 22 AA.

XX AC AAW66127;

XX XX 17-NOV-1998 (first entry)  
XX XX Prosapoin receptor agonist #1.

DE XX prosapoin; receptor agonist; neuropathic pain; neurite outgrowth;  
KW KW neural cell death; nerve disorder; side effect.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9839357-A1.

XX XX 11-SEP-1998.

XX XX 11-SEP-1997; 97WO-US16062.

XX PR 05-MAR-1997; 97WO-US04143.

XX PA (REGC ) UNIV CALIFORNIA.

XX O'Brien JS;  
 XX WPI; 1998-495790/42.  
 DR N-PSDB; AAV07664.  
 XX  
 XX Use of prosaposin receptor agonists - for alleviating neuropathic  
 PT pain, inhibiting sensory or motor neuropathy, or inhibiting neural  
 PT cell death  
 XX  
 XX Claim 3; Page 2; 67pp; English.  
 PS  
 XX The invention relates to prosaposin receptor agonists. Also claimed  
 CC are: (1) methods for alleviating neuropathic pain or inhibiting the  
 CC onset of neuropathic pain, comprising administering a prosaposin receptor  
 CC agonist; (2) inhibiting sensory or motor neuropathy, comprising  
 CC contacting neuronal cells with a composition comprising a prosaposin  
 CC receptor agonist; (3) methods for stimulating neurite outgrowth,  
 CC inhibiting neural cell death, promoting myelination, or inhibiting  
 CC demyelination comprising contacting neuronal cells with a composition  
 CC comprising a prosaposin receptor agonist which has 14-50 amino acids and  
 CC comprises the sequence of a prosaposin derived protein. The processes  
 CC may be used for treatment of neuropathic pain resulting from peripheral  
 CC nerve disorders (e.g. neuroma, nerve compression, nerve crush, nerve  
 CC stretch, incomplete nerve transection, mononeuropathy or polyneuropathy)  
 CC or disorders of dorsal root ganglia, the spinal cord, the brainstem, the  
 CC thalamus or the cortex. The receptor agonists do not cause undesirable  
 CC side effects. The present sequence represents a specifically claimed  
 CC prosaposin receptor agonist.  
 XX  
 XX Sequence 22 AA;  
 SQ  
 Query Match 46.6%; Score 61; DB 19; Length 22;  
 Best Local Similarity 60.0%; Pred. No. 0.0012;  
 Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 6 CEXXXKEXKXXDNNKXKE 25  
 DB 1 CEFLVKEVTKLIDNNKTEKE 20  
 RESULT 15  
 AA085656  
 ID AA085656 standard; Peptide; 22 AA.  
 AC  
 AC AA085656;  
 XX  
 XX 19-JUL-1999 (first entry)  
 DT  
 XX Prosaposin receptor agonist.  
 DE  
 XX Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
 KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
 KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
 KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
 KW inflammation; rheumatoid arthritis; Crohn's disease;  
 KW irritable bowel syndrome; asthma; cardiac infarction;  
 KW congestive heart failure; multiple sclerosis;  
 KW acute disseminated inflammatory leukoencephalitis;  
 KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
 KW Parkinson's disease; amyotrophic lateral sclerosis;  
 KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
 KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
 KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX W09912559-A1.  
 PN  
 XX  
 XX 18-MAR-1999.  
 PD  
 XX  
 XX 09-SEP-1998; 98WO-US19216.  
 PF  
 XX

PR 04-JUN-1998; 98US-0088129.  
 PR 09-SEP-1997; 97US-0058352.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI O'Brien JS;  
 XX  
 DR WPI; 1999-229139/19.  
 XX  
 XX Use of prosaposin receptor agonist  
 PT  
 XX Claim 7; Page 66; 90pp; English.  
 PS  
 XX Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
 CC to generate saposins A, B, C and D, all of which are similar to each  
 CC other and have a similar placement of six cysteines, a glycosylation  
 CC site and conserved proline residues. Prosaposin, saposin C and  
 CC prosaposin derived peptides (prosaptides), have therapeutic  
 CC applications in promoting recovery after toxic, traumatic, myocardial  
 CC ischaemic, degenerative and inherited lesions to the peripheral and  
 CC central nervous system. Prosaposin receptor agonists (PRAs)  
 CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
 CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
 CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
 CC members which inhibit caspases, thereby inhibiting apoptosis. An  
 CC additional mechanism whereby PRAs inhibit apoptosis is by blocking  
 CC activation of JNK, a proapoptotic signaling component. Within  
 CC several minutes after binding to the receptor, PRAs block JNK  
 CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
 CC activation of JNK by TNF alpha is another well known mechanism for  
 CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
 CC apoptosis. The method can be used for inhibiting apoptosis which is  
 CC caspase-mediated or induced by a proinflammatory cytokine, for  
 CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
 CC apoptosis associated with a disorder such as e.g. rheumatoid  
 CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
 CC infarction, congestive heart failure, multiple sclerosis, acute  
 CC disseminated inflammatory leukoencephalitis, progressive multifocal  
 CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
 CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
 CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
 CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
 CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
 CC liver disease. This peptide corresponds to amino acids 8 to 29 of  
 CC human saposin C (See AA085653) and acts as a prosaposin receptor  
 CC agonist.  
 XX  
 XX Sequence 22 AA;  
 SQ  
 Query Match 46.6%; Score 61; DB 20; Length 22;  
 Best Local Similarity 60.0%; Pred. No. 0.0012;  
 Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 6 CEXXXKEXKXXDNNKXKE 25  
 DB 1 CEFLVKEVTKLIDNNKTEKE 20  
 Search completed: June 2, 2003, 14:15:45  
 Job time : 30.7179 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 13.641 Seconds  
(without alignments)  
267.803 Million cell updates/sec

Title: US-09-780-438C-6

Perfect score: 131

Sequence: 1 XXCEXEXXKEXXKXXNNKXEXXDXDXKXKXXK 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	77.1	527	1 SAHUP	saposin precursor
2	84	64.1	80	2 S21770	saposin-C - bovine
3	61	46.6	81	2 A32026	glucosylceramide b
4	46	35.1	554	1 A28716	saposin precursor
5	43	32.8	557	1 JH0604	saposin precursor
6	43	32.8	913	2 T46339	hypothetical prote
7	43	32.8	1216	2 A28822	1-phosphatidylinos
8	43	32.8	1216	2 A28821	1-phosphatidylinos
9	42	32.1	314	2 T15674	hypothetical prote
10	42	32.1	483	2 S41853	centromere/microtu
11	42	32.1	985	2 T00207	P109 protein - sil
12	42	32.1	2285	2 T12796	probable transglyc
13	41.5	31.7	473	2 T70031	cell wall-binding
14	41	31.3	419	2 T18450	hypothetical prote
15	40	30.5	191	1 H69472	iron-dependent rep
16	40	30.5	301	2 T33068	hypothetical prote
17	40	30.5	347	2 T39392	hypothetical prote
18	40	30.5	519	2 S54014	hypothetical prote
19	40	30.5	570	2 T08778	hypothetical prote
20	40	30.5	731	2 H86132	hypothetical prote
21	40	30.5	735	2 G91290	hypothetical prote
22	39.5	30.2	165	2 T52114	probable transcrip
23	39.5	30.2	263	2 G87721	protein ZC123.3 [1
24	39.5	30.2	1377	2 T19214	UDP-glucose-glycop
25	39	29.8	189	2 S44639	hypothetical prote
26	39	29.8	210	2 T28771	hypothetical prote
27	39	29.8	211	2 T25911	hypothetical prote
28	39	29.8	315	2 T16874	hypothetical prote
29	39	29.8	572	2 T20764	hypothetical prote

type III DNA modif  
1-phosphatidylinos  
hypothetical prote  
rifin PB80040c - m  
hypothetical prote  
chromatinic RING f  
hypothetical prote  
hypothetical prote  
hypothetical prote  
SPT6 protein - yea  
variant-specific s  
quak-type molecula  
fumarate reductase  
dnak-type molecula  
sperm tail-specifi  
85K major surface

#### ALIGNMENTS

##### RESULT 1

###### SAHUP

saposin precursor [validated] - human

N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon  
ein (SAP); sphingolipid activator protein A2; sulfate sulfate activator protein  
N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D  
C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence.revision 17-Nov-1995 #text.change 08-Dec-2000  
C:Accession: JX0061; A57368; A42003; B42003; C42003; D42003; A30367; S34740; S36140;  
O226; I37265; I37264

J:Nakano, T.; Sandhoff, K.; Stuenkel, J.; Christomanou, H.; Suzuki, K.

J:Biochem. 105, 152-154, 1989

A:Title: Structure of full-length cDNA coding for sulfate activator, a Co-beta-gluc

A:Reference number: JX0061; MUID:89255151; PMID:2458298

A:Accession: JX0061

A:Molecule type: mRNA

A:Residues: 1-527 <NAK>

A:Cross-references: GB:D00422; NID:g220063; PIDN:BAA00321.1; PID:g220064

A:Note: alternative splice form 1

A:Accession: A57368

A:Molecule type: mRNA

A:Residues: 1-259,263-527 <NA2>

A:Cross-references: GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59494.1; PID:g337756

A:Note: alternative splice form 2

R:Rorman, E.G.; Scheinker, V.; Grabowski, G.A.

Genomics 13, 312-318, 1992

A:Title: Structure and evolution of the human prosaposin chromosomal gene.

A:Reference number: A42003; MUID:92307663; PMID:1612590

A:Accession: A42003

A:Molecule type: DNA

A:Residues: 50-140 <ROR>

A:Cross-references: GB:M86181

A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)

A:Accession: B42003

A:Molecule type: DNA

A:Residues: 185-259;263-276 <RO2>

A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)

A:Accession: C42003

A:Molecule type: DNA

A:Residues: 305-393 <RO3>

A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence

A:Accession: D42003

A:Molecule type: DNA

A:Residues: 399-487 <RO4>

A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence

R:Rorman, E.G.; Grabowski, G.A.

Genomics 5, 486-492, 1989

A:Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sp

A:Reference number: A30367; MUID:90129043; PMID:2515150

A:Accession: A30367

A:Molecule type: mRNA

A:Residues: 1-259,263-527 <RO5>

A;Cross-references: GB:J03077; NID:g183230; PIDN:AAA52560.1; PID:g183231  
A;Note: alternative splice form 2  
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Biochem. Biophys. 304, 110-116, 1993  
A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor of ceramide sulfate  
A;Reference number: S34740; MUID:93311991; PMID:8323276  
A;Accession: S34740  
A;Molecule type: protein  
A;Residues: 17-24;165-172;180-189;301-305 <HIR>  
R;Tyynelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M. FEBS Lett. 330, 8-12, 1993  
A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.  
A;Reference number: S36140; MUID:93380576; PMID:8370464  
A;Accession: S36140  
A;Molecule type: protein  
A;Residues: 'XX', 62, 'X', 64-65, 'X', 67-79, 'X', 81-84 <TY>  
A;Note: saposin A  
A;Accession: S36141  
A;Molecule type: protein  
A;Residues: 'XXX', 413-414, 'X', 416-428, 'X', 430-434 <TY2>  
R;Holtzman, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K. J. Biol. Chem. 266, 7586-7590, 1991  
A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs and a precursor  
A;Reference number: S36988; MUID:91210267; PMID:2019586  
A;Accession: S36988  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-527 <HOL>  
A;Cross-references: EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PID:g337760  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative splicing  
A;Accession: S36989  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-259, 263-527 <HO2>  
A;Cross-references: EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PID:g337765  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative splicing  
A;Accession: S36990  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-259, 261-527 <HO3>  
A;Cross-references: EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PID:g337767  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative splicing  
R;Kondoh, K.; Hineno, T.; Sano, A.; Kakimoto, Y. Biochem. Biophys. Res. Commun. 181, 286-292, 1991  
A;Title: Isolation and characterization of prosaposin from human milk.  
A;Reference number: PS0330; MUID:92068206; PMID:1958198  
A;Accession: PS0330  
A;Molecule type: protein  
A;Residues: 17-24, 'X', 26 <KON>  
A;Experimental source: milk  
R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990  
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosylation defect  
A;Reference number: A35985; MUID:90207231; PMID:2320574  
A;Accession: A35985  
A;Molecule type: mRNA  
A;Residues: 213-221 <KRE>  
A;Cross-references: GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:g337762  
A;Accession: M32221  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-259, 263-527 <KR2>  
A;Cross-references: GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:g337762  
A;Experimental source: lymphoblast  
A;Accession: C35985  
A;Molecule type: mRNA  
A;Residues: 213-216, 'I', 218-221 <KR3>  
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; th  
R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.

Eur. J. Biochem. 192, 709-714, 1990  
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein  
A;Reference number: S13195; MUID:9106165; PMID:2209618  
A;Accession: S13196  
A;Molecule type: protein  
A;Residues: 195-259, 263-277 <FUE>  
R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y. Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989  
A;Title: Saposin A: second cerebroside activator protein.  
A;Reference number: A32784; MUID:89240739; PMID:2717620  
A;Accession: A32784  
A;Molecule type: protein  
A;Residues: 60-84;86-107;109-119;125-134 <MOR>  
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L. Science 241, 1098-1101, 1988  
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same gene  
A;Reference number: A41240; MUID:88321660; PMID:2842863  
A;Accession: A41240  
A;Molecule type: mRNA  
A;Residues: 'GSSR', 18-259, 263-299, 'D', 301-302, 'D', 304-527 <OAB>  
A;Cross-references: GB:J03086  
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987  
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein  
A;Reference number: S02289; MUID:88068647; PMID:2825202  
A;Accession: S02289  
A;Status: significant sequence differences  
A;Molecule type: mRNA  
A;Cross-references: EMBL:U03015  
A;Note: this sequence corrected by A41240  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 369, 1361-1365, 1988  
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator prote  
A;Reference number: S02028; MUID:89207118; PMID:3242555  
A;Accession: S02028  
A;Molecule type: protein  
A;Residues: 195-259, 263-276 <KLE>  
R;Fuerst, W.; Machleidt, W.; Sandhoff, K. Biol. Chem. Hoppe-Seyler 369, 317-328, 1988  
A;Title: The precursor of sulfatide activator protein is processed to three different  
A;Reference number: S00813; MUID:89000190; PMID:3048308  
A;Accession: S00813  
A;Molecule type: protein  
A;Residues: 410-487 <F02>  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987  
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occur  
A;Reference number: S00226; MUID:88163077; PMID:3442600  
A;Accession: S00226  
A;Molecule type: protein  
A;Residues: 314-393 <KL2>  
R;Vaccaro, A.M.; Salvio, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Sicilia J. Biol. Chem. 270, 9933-9960, 1995  
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide b  
A;Reference number: A57297; MUID:95247790; PMID:7730378  
R;Holtzman, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K. FEBS Lett. 280, 267-270, 1991  
A;Title: The organization of the gene for the human cerebroside sulfate activator pro  
A;Reference number: I37264; MUID:91192146; PMID:2013321  
A;Accession: I37265  
A;Status: translated  
A;Molecule type: DNA  
A;Residues: 59-125 <RES>  
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A;Accession: I37264  
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A;Cross-references: EMBL:X57108; NID:g30233; PIDN:CAA40392.1; PID:g1565257  
A;Note: sequence revised relative to PID:g30233 (corrected coding region)  
C;Genetics;



A: Accession: A39236  
A: Molecule type: protein  
A: Residues: 879-889 <R1>  
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F: 318-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homology  
A: Accession: A39236  
A: Molecule type: protein  
A: Residues: 879-889 <R1>  
C: Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homology  
F: 318-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homology

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Best local Similarity 26.9%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
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C:Species: *Bacillus subtilis* phage *SPBc2*  
C:date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 15-Oct-1999  
C:Accession: T12796; A69911  
R:Lazarevic, V.; Duestarhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.  
submitted to the EMBL Data Library, August 1997  
A:Description: The complete nucleotide sequence of the *Bacillus subtilis* SPBc2 pro  
A:Reference number: Z17583  
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A:Status: translated from GB/EMBL/DBJ  
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R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
A.: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gal  
le, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardino  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl  
A:Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumslein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: A69911  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
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A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yomI

Query Match 32.1%; Score 42; DB 2; Length 2285;  
Best Local Similarity 38.5%; Pred. No. 57;  
Matches 10; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

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RESULT 13  
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C:date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999  
C:Accession: F70031  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
A.: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gal  
le, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardino  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl  
A:Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumslein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: F70031  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-473 <KUN>  
A:Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15485.1; PID:ell1861

A:Experimental source: strain 168

C:Genetics:

A:Gene: yvce

Query Match 31.7%; Score 41.5; DB 2; Length 473;  
Best Local Similarity 40.7%; Pred. No. 19;  
Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 7 EXXXKXXKXND-NKXKEXDXDXK 32

Db 52 EAKEKELTELQENQSKIEKELKDINDK 78

#### RESULT 14

Tl8450

hypothetical protein C0570c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2002

C:Accession: Tl8450

R:Lawson, D.; Bowman, S.; Barrell, B.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z18937

A:Accession: Tl8450

A>Status: preliminary; translated from GE/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-419 <LAW>

A:Cross-references: EMBL:AL008970; NID:e1407852; PIDN:CAA15592.1

C:Genetics:

A:Map position: 3

A:Introns: 15/3; 169/1

A:Note: C0570c

Query Match 31.3%; Score 41; DB 2; Length 419;  
Best Local Similarity 29.0%; Pred. No. 21;  
Matches 9; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 4 EXCEXXKXXKXNDNNKXKEXDXDXKXC 34

Db 291 EECKERYKEDCKEDKEDKCKEKGKKEC 321

#### RESULT 15

H69472

Iron-dependent repressor homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C:Accession: H69472

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: H69472

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-191 <KLE>

A:Cross-references: GB:AE000979; GB:AE000782; NID:g2689302; PIDN:AAE89462.1; PID:g264878

C:Superfamily: conserved hypothetical protein MJ0568

Query Match 30.5%; Score 40; DB 1; Length 191;  
Best Local Similarity 34.8%; Pred. No. 16;  
Matches 8; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 3 CEXCEXXKEXKXNDNNKXKE 25

Db 121 CEVCECTQRYLSLSDATEGEYE 143

Search completed: June 2, 2003, 14:16:20

Job time : 14.641 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	101	77.1	524	1	SAP_HUMAN
2	87	66.4	525	1	SAP_BOVIN
3	61	46.6	81	1	SAP_CAVPO
4	58	44.3	518	1	SAP_CHICK
5	56	35.1	554	1	SAP_RAT
6	43	32.8	557	1	SAP_MOUSE
7	43	32.8	1216	1	P1B1_BOVIN
8	43	32.8	1216	1	P1B1_RAT
9	43	32.8	1216	1	P1B1_RAT
10	42	32.1	483	1	CBF5_YEAST
11	42	32.1	574	1	TACY_STRCB
12	42	32.1	574	1	TACY_STROB
13	41.5	31.7	471	1	YVCE_BACSU
14	40	30.5	519	1	YMP4_YEAST
15	39	29.8	189	1	YPT2_CAEEL
16	39	29.8	572	1	NH25_CAEEL
17	38	29.0	474	1	CBF5_KLULA
18	38	29.0	1048	1	Z217_HUMAN
19	38	29.0	1451	1	SPT6_YEAST
20	37.5	28.6	489	1	Y092_METYA
21	37.5	28.6	666	1	B1P_LYCES
22	37.5	28.6	668	1	B1P5_TOBAC
23	37.5	28.6	1391	1	MST2_DROHY
24	37	28.2	238	1	NEUM_HUMAN
25	37	28.2	373	1	ACT_CHOCR
26	37	28.2	375	1	DEK_HUMAN
27	37	28.2	472	1	Z1N3_HUMAN
28	37	28.2	524	1	YB18_YEAST
29	37	28.2	846	1	CLOC_HUMAN
30	37	28.2	855	1	CLOC_MOUSE
31	37	28.2	886	1	H897_STREFF
32	36.5	27.9	669	1	B1P2_ARATHY
33	36.5	27.9	669	1	B1P1_ARATHY

RA Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).  
[6] PARTIAL SEQUENCE OF 60-142.  
RX MEDLINE-89240739; PubMed-2717620;  
RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,  
Kishimoto Y.;  
RT "Saposin A: second cerebroside activator protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).  
[7] SEQUENCE OF 195-263 FROM N.A.  
RX MEDLINE-86130593; PubMed-2868718;  
RA Dewji N.M., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,  
Hill F., O'Brien J.S.;  
RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),  
the sulfatide sulfatase activator.";  
RL Biochem. Biophys. Res. Commun. 134:989-994(1986).  
[8] SEQUENCE OF 195-274.  
RX MEDLINE-89207118; PubMed-3242555;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence of the naturally occurring A2 activator  
protein for enzymic sphingomyelin degradation: identity to the  
sulfatide activator protein (SAP-1).";  
RL Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).  
[9] SEQUENCE OF 311-390.  
RX MEDLINE-88163077; PubMed-3442600;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence and carbohydrate content of the  
naturally occurring glucosylceramide activator protein (A1 activator)  
absent from a new human Gaucher disease variant.";  
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).  
[10] SEQUENCE OF 407-484.  
RX MEDLINE-89000190; PubMed-3048308;  
RA Furst W., Machleidt W., Sandhoff K.;  
RT "The precursor of sulfatide activator protein is processed to three  
different proteins.";  
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).  
[11] PARTIAL SEQUENCE OF 405-484.  
RX MEDLINE-89025876; PubMed-2845979;  
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;  
RT "Saposin D: a sphingomyelinase activator.";  
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).  
[12] SEQUENCE OF 17-26.  
RX MEDLINE-92068206; PubMed-1958198;  
RA Kondoh K., Hinenio T., Sano A., Kakimoto Y.;  
RT "Isolation and characterization of prosaposin from human milk.";  
RL Biochem. Biophys. Res. Commun. 181:286-292(1991).  
[13] PARTIAL SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.  
RX MEDLINE-20032116; PubMed-10562467;  
RA Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.,  
Waring A.J., To T., Fluharty C.B., Paull K.F.;  
RT "Preparation of the cerebroside sulfate activator (CSA or saposin B)  
from human urine.";  
RL Mol. Genet. Metab. 68:391-403(1999).  
[14] TISSUE-urine;  
RX MEDLINE-90147748; PubMed-2302219;  
RA Rafi M.A., Zhang X.-L., Pegala G., Wenger D.A.;  
RT "Detection of a point mutation in sphingolipid activator protein-1  
mRNA in patients with a variant form of metachromatic  
leukodystrophy.";  
RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).  
[15] SEQUENCE FROM N.A., AND VARIANT MLD ILB-217.  
RX MEDLINE-90207231; PubMed-2320574;  
RA Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluharty A.L.,  
O'Brien J.S.;  
RT "Characterization of a mutation in a family with saposin B  
deficiency: a glycosylation site defect.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).  
[16] VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE-91210267; PubMed-2019586;  
RA Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,  
Suzuki K.;  
RT "Sulfatide activator protein. Alternative splicing that generates  
three mRNAs and a newly found mutation responsible for a clinical  
disease.";  
RL J. Biol. Chem. 266:7556-7560(1991).  
[17] VARIANT GAUCHER PHE-388.  
RX MEDLINE-91285107; PubMed-2060627;  
RA Schnabel D., Schroeder M., Sandhoff K.;  
RT "Mutation in the sphingolipid activator protein 2 in a patient with a  
variant of Gaucher disease.";  
RL FEBS Lett. 284:57-59(1991).  
[18] REVIEW ON MLD VARIANTS.  
RX MEDLINE-95170731; PubMed-7866401;  
RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;  
RT "Molecular genetics of metachromatic leukodystrophy.";  
RL Hum. Mutat. 4:233-242(1994).  
[19] FUNCTION: The lysosomal degradation of sphingolipids takes place  
by the sequential action of specific hydrolases. Some of these  
enzymes require specific low-molecular mass, non-enzymic proteins:  
the sphingolipids activator proteins (coproteins).  
[20] FUNCTION: Saposin A and saposin C stimulate the hydrolysis of  
glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and  
galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).  
Saposin C apparently acts by combining with the enzyme and acidic  
lipid to form an activated complex, rather than by solubilizing  
the substrate.  
[21] FUNCTION: Saposin B stimulates the hydrolysis of galacto-  
cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1  
gangliosides by beta-galactosidase (EC 3.2.1.23) and  
globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).  
Saposin B forms a solubilizing complex with the substrates of the  
sphingolipid hydrolases.  
[22] FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase  
activator (EC 3.1.4.12).  
[23] SUBUNIT: Saposin B is a homodimer.  
[24] SUBCELLULAR LOCATION: Lysosomal.  
[25] ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),

RA Stevens R.L., Fluharty C.B., Fluharty A.L.;  
RT "Structure of the asparagine-linked sugar chains of porcine kidney and  
human urine cerebroside sulfate activator protein.";  
RL J. Mass Spectrom. 35:1416-1424(2000).  
[16] MASS SPECTROMETRY.  
RX TISSUE-urine;  
RA Paull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,  
Kutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,  
Fluharty C.B., Fluharty A.L.;  
RT "Cerebroside sulfate activator protein (Saposin B): chromatographic  
and electrospray mass spectrometric properties.";  
RL J. Mass Spectrom. 34:1040-1054(1999).  
[17] VARIANT MLD ILB-217.  
RX MEDLINE-90147748; PubMed-2302219;  
RA Rafi M.A., Zhang X.-L., Pegala G., Wenger D.A.;  
RT "Detection of a point mutation in sphingolipid activator protein-1  
mRNA in patients with a variant form of metachromatic  
leukodystrophy.";  
RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).  
[18] SEQUENCE FROM N.A., AND VARIANT MLD ILB-217.  
RX MEDLINE-90207231; PubMed-2320574;  
RA Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluharty A.L.,  
O'Brien J.S.;  
RT "Characterization of a mutation in a family with saposin B  
deficiency: a glycosylation site defect.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).  
[19] VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE-91210267; PubMed-2019586;  
RA Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,  
Suzuki K.;  
RT "Sulfatide activator protein. Alternative splicing that generates  
three mRNAs and a newly found mutation responsible for a clinical  
disease.";  
RL J. Biol. Chem. 266:7556-7560(1991).  
[20] VARIANT GAUCHER PHE-388.  
RX MEDLINE-91285107; PubMed-2060627;  
RA Schnabel D., Schroeder M., Sandhoff K.;  
RT "Mutation in the sphingolipid activator protein 2 in a patient with a  
variant of Gaucher disease.";  
RL FEBS Lett. 284:57-59(1991).  
[21] REVIEW ON MLD VARIANTS.  
RX MEDLINE-95170731; PubMed-7866401;  
RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;  
RT "Molecular genetics of metachromatic leukodystrophy.";  
RL Hum. Mutat. 4:233-242(1994).  
[19] FUNCTION: The lysosomal degradation of sphingolipids takes place  
by the sequential action of specific hydrolases. Some of these  
enzymes require specific low-molecular mass, non-enzymic proteins:  
the sphingolipids activator proteins (coproteins).  
[20] FUNCTION: Saposin A and saposin C stimulate the hydrolysis of  
glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and  
galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).  
Saposin C apparently acts by combining with the enzyme and acidic  
lipid to form an activated complex, rather than by solubilizing  
the substrate.  
[21] FUNCTION: Saposin B stimulates the hydrolysis of galacto-  
cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1  
gangliosides by beta-galactosidase (EC 3.2.1.23) and  
globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).  
Saposin B forms a solubilizing complex with the substrates of the  
sphingolipid hydrolases.  
[22] FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase  
activator (EC 3.1.4.12).  
[23] SUBUNIT: Saposin B is a homodimer.  
[24] SUBCELLULAR LOCATION: Lysosomal.  
[25] ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),







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EMBL; S36200; AAB22175.1; -  
EMBL; S71616; AAB31059.1; -  
EMBL; U27340; AAA92567.1; -  
EMBL; U57999; AAB02695.1; -  
MGD; MGI:97783; Reap.  
InterPro: IPR003119; Sapa.  
InterPro: IPR000004; Sapa.  
Pfam: PF02199; Sapa; 2.  
ProDom: PD001732; Sapa; 4.  
SMART: SM00162; Sapa; 2.  
SMART: SM00118; Sapa; 4.  
Signal; Signal; Glycoprotein; Repeat.  
FT SIGNAL 1 16 BY SIMILARITY.  
FT CHAIN 17 557 SULFATED GLYCOPROTEIN 1.  
FT DOMAIN 21 54 SAPOSIN-LIKE TYPE A 1.  
FT DOMAIN 59 142 SAPOSIN-LIKE TYPE B 1.  
FT DOMAIN 193 277 SAPOSIN-LIKE TYPE B 2.  
FT DOMAIN 313 394 SAPOSIN-LIKE TYPE B 3.  
FT DOMAIN 438 519 SAPOSIN-LIKE TYPE B 4.  
FT DOMAIN 524 557 SAPOSIN-LIKE TYPE A 2.  
FT DISULFID 63 138 BY SIMILARITY.  
FT DISULFID 66 132 BY SIMILARITY.  
FT DISULFID 94 106 BY SIMILARITY.  
FT DISULFID 197 273 BY SIMILARITY.  
FT DISULFID 200 267 BY SIMILARITY.  
FT DISULFID 229 240 BY SIMILARITY.  
FT DISULFID 317 390 BY SIMILARITY.  
FT DISULFID 320 384 BY SIMILARITY.  
FT DISULFID 348 359 BY SIMILARITY.  
FT DISULFID 442 515 BY SIMILARITY.  
FT DISULFID 445 509 BY SIMILARITY.  
FT DISULFID 473 484 BY SIMILARITY.  
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 83 83 Q -> E (IN REF. 2).  
FT CONFLICT 158 158 I -> V (IN REF. 3).  
FT CONFLICT 160 160 MISSING (IN REF. 2).  
FT CONFLICT 171 172 MS -> SA (IN REF. 3).  
FT CONFLICT 244 244 V -> L (IN REF. 2).  
FT CONFLICT 254 254 M -> I (IN REF. 3).  
FT CONFLICT 255 255 L -> W (IN REF. 2).  
FT CONFLICT 260 262 MISSING (IN REF. 3).  
FT CONFLICT 307 307 N -> D (IN REF. 2).  
FT CONFLICT 322 322 F -> L (IN REF. 2).  
FT CONFLICT 349 350 AL -> GV (IN REF. 1).  
FT CONFLICT 367 367 G -> D (IN REF. 3).  
FT CONFLICT 370 370 L -> Q (IN REF. 2).  
FT CONFLICT 373 373 I -> D (IN REF. 3).  
FT CONFLICT 391 391 I -> T (IN REF. 3).  
FT CONFLICT 393 393 R -> L (IN REF. 3).  
FT CONFLICT 406 406 A -> R (IN REF. 2 AND 3).  
FT CONFLICT 430 430 P -> R (IN REF. 2).  
FT CONFLICT 440 440 C -> F (IN REF. 3).  
FT CONFLICT 445 445 C -> F (IN REF. 3).  
FT CONFLICT 448 448 L -> P (IN REF. 4).  
SQ SEQUENCE 557 AA; 61422 MW; 134593E20499E35E CRC64;

Query Match 32.8%; Score 43; DB 1; Length 557;

Best Local Similarity 21.9%; Pred. No. 4.9;  
Matches 7; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 3 CEVCEXXXEXXKXNNKXEXXKXDXKXC 34

Db 63 CDICKTVVTVAGNLLKDNATQBEILHYLEKTC 94

RESULT 7

PIBL\_BOVIN  
ID P1BL\_BOVIN STANDARD; PRT; 1216 AA.  
AC P10894;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1  
DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-1) (PLC-154).  
GN PLCB1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=88270496; PubMed=2455601;  
RA Katan M., Kriz R.W., Totty N., Philip R., Meldrum E., Aldape R.A.,  
RA Knopf J.L., Parker P.J.;  
RT "determination of the primary structure of PLC-154 demonstrates  
RT diversity of phosphoinositide-specific phospholipase C activities.";  
RL Cell 54:171-177(1988).  
CC -|- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES  
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS  
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE  
CC C ENZYMES.  
CC -|- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-  
CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +  
CC diacylglycerol.  
CC -|- COFACTOR: Calcium.  
CC -|- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS  
CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.  
CC -|- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS  
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.  
CC -|- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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EMBL; J03137; AAA30702.1; -  
DR PIR; A28822; A28822.  
DR HSSP; P10688; 1DJX.  
DR InterPro: IPR000008; C2.  
DR InterPro: IPR001192; PI\_PLC.  
DR InterPro: IPR000909; PI\_PLC\_Xdom.  
DR InterPro: IPR001711; PI\_PLC\_Y.  
DR Pfam; PF00168; C2; 1.  
DR Pfam; PF00387; PI-PLC-Y; 1.  
DR Pfam; PF00388; PI-PLC-X; 1.  
DR PRINTS; PR00390; PHPLIPASEC.  
DR ProDom; PD001202; PI\_PLC\_Y; 1.  
DR SMART; SM00239; C2; 1.  
DR SMART; SM00148; PLCXC; 1.  
DR SMART; SM00149; PLCYC; 1.  
DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
DR PROSITE; PS50007; PIPLC\_X\_DOMAIN; 1.  
DR PROSITE; PS50008; PIPLC\_Y\_DOMAIN; 1.  
DR Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium.  
FT DOMAIN 316 467 DOMAIN X.  
FT DOMAIN 540 656 DOMAIN Y.  
FT DOMAIN 663 761 C2 DOMAIN.  
FT ACT\_SITE 331 331 BY SIMILARITY.  
FT ACT\_SITE 378 378 BY SIMILARITY.  
FT MOD\_RES 887 887 PHOSPHORYLATION (BY PKC).  
SQ SEQUENCE 1216 AA; 138714 MW; BEF809177F1B7ABB CRC64;

Query Match 32.8%; Score 43; DB 1; Length 1216;  
Best Local Similarity 42.9%; Pred. No. 10;



Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKXXKXNDNNKXK 24  
 ||| ||| | : ||

Db 1059 EICEKELKKKKKKRQEK 1079

## RESULT 8

PIB1\_HUMAN  
 ID PIB1\_HUMAN STANDARD; PRT; 1216 AA.  
 AC Q9NQ66; Q9NQ65; Q9NQ59; Q9NTH4; O60325; Q9H4H2; Q9BQW2; Q9UJP6;  
 AC Q9UM26;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1  
 DE EC 3.1.4.11 (PLC-beta-1) (Phospholipase C-beta-1) (PLC-1) (PLC-154).  
 GN PLCB1 OR KIAA0581.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
 RC TISSUE=Brain;  
 RX PubMed=11118617;  
 RA Caricasole A., Sala C., Roncarati R., Formenti E., Terstappen G.C.;  
 RA "Cloning and characterization of the human phosphoinositide-specific  
 RT phospholipase C-beta 1 (PLCbetal)."  
 RL Biochim. Biophys. Acta 1517:63-72(2000).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC TISSUE=Brain;  
 RX MEDLINE=20225428; PubMed=10760467;  
 RA Peruzzi D., Calabrese G., Faenza I., Manzoli L., Matteucci A.;  
 RA Gianfrancesco F., Billi A.M., Stuppia L., Palka G., Cocco L.;  
 RT "Identification and chromosomal localisation by fluorescence in situ  
 RT hybridisation of human gene of phosphoinositide-specific phospholipase  
 RT C beta 1.";  
 RL Biochim. Biophys. Acta 1484:175-182(2000).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagdley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Connor R.E.,  
 RA Clegg S., Cobley V.E., Collier R.E., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Levasialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.D., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,  
 RA Skuce C.M., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilmberg L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 [4]  
 RP SEQUENCE OF 261-1216 FROM N.A. (ISOFORM B).  
 RC TISSUE=Testis;

RA Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 519-1216 FROM N.A. (ISOFORM A).  
 RC TISSUE=Brain;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES  
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS  
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE  
 CC C ENZYMES.  
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-D-myo-inositol 4,5-  
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +  
 CC diacylglycerol.  
 CC -1- COFACTOR: Calcium.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS  
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.  
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS  
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; AJ278313; CAB98142.1; -  
 DR EMBL; AJ278314; CAB98143.1; -  
 DR EMBL; AY004175; AAF86613.1; -  
 DR EMBL; AL031683; CAC16181.1; -  
 DR EMBL; AL031683; CAC34366.1; -  
 DR EMBL; AL050315; CAB56498.1; -  
 DR EMBL; AL049632; CAB46663.1; -  
 DR EMBL; AL137267; CAB70666.1; -  
 DR EMBL; AB011153; BAA25507.1; -  
 DR HGSP; P10688; IDJX.  
 DR Genew; HGNC:15917; PLCB1.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR001192; PI\_PLC.  
 DR InterPro; IPR000909; PI\_PLC\_Xdom.  
 DR InterPro; IPR001711; PI\_PLC\_Y.  
 DR Pfam; PF00168; C2; 2.  
 DR Pfam; PF00387; PI\_PLC-Y; 3.  
 DR Pfam; PF00388; PI\_PLC-X; 2.  
 DR PRINTS; PR00390; PHPLIPASEC.  
 DR PRODOM; PD001202; PI\_PLC\_Y; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00148; PLCXG; 1.  
 DR SMART; SM00149; PLCYC; 1.  
 DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
 DR PROSITE; PS50007; PIPIC\_X\_DOMAIN; 1.  
 DR PROSITE; PS50008; PIPIC\_Y\_DOMAIN; 1.  
 KW Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium;  
 KW Alternative splicing.  
 FT DOMAIN 316 467  
 FT DOMAIN 540 656  
 FT DOMAIN 663 761  
 FT ACT\_SITE 331 331  
 FT ACT\_SITE 378 378  
 FT MOD\_RES 887 887  
 FT VARSPIC 1142 1216

```
FT FT CONFLICT 1 34 189 189 B).
FT FT MAGAOPVHALOLKPCVSDSLKKGFKVKWDDD -> MGS
FT FT LOGIATVKILIRILSDALIRKETDLKS (IN REF. 2).
FT FT L -> M (IN REF. 2).
FT FT CONFLICT 203 216 L -> L (IN REF. 2).
FT FT CONFLICT 216 216 L -> F (IN REF. 2).
FT FT CONFLICT 221 221 P -> L (IN REF. 2).
FT FT CONFLICT 266 266 L -> P (IN REF. 2).
FT FT CONFLICT 309 309 P -> T (IN REF. 2).
FT FT CONFLICT 320 320 Q -> R (IN REF. 2).
FT FT CONFLICT 352 352 V -> A (IN REF. 2).
FT FT CONFLICT 366 366 K -> R (IN REF. 2).
FT FT CONFLICT 393 393 E -> K (IN REF. 2).
FT FT CONFLICT 983 983 P -> S (IN REF. 1; CAB98143).
SQ SEQUENCE 1216 AA; 138566 MW; 6P4263DIA50C6FDI CRC64;

Query Match 32.8%; Score 43; DB 1; Length 1216;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXKXNDNNKXK 24
DB 1059 EICEKEKELKKMKKKRQEK 1079

RESULT 9
PIBL_RAT STANDARD; PRT; 1216 AA.
AC P10687;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
DE (EC 3.1.4.11) (PLC-beta-1) (phospholipase C-beta-1) (PLC-1) (PLC-154).
GN PLCB1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88270495; PubMed=3390863;
RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
RT "Cloning and sequence of multiple forms of phospholipase C.";
RL Cell 54:161-169(1988).
RN [2]
RP ACTIVITY, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RX MEDLINE=93203266; PubMed=8454637;
RA Jhon D.-Y., Lee H.-H., Park D., Lee C.-W., Lee K.-H., Yoo O.J.,
RA Rhee S.G.;
RT "Cloning, sequencing, purification, and Gq-dependent activation of
RT phospholipase C-beta 3.";
RL J. Biol. Chem. 268:6654-6661(1993).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -1- COFACTOR: Calcium.
CC -1- SUBCELLULAR LOCATION: Cytosolic and particulate fractions.
CC -1- TISSUE SPECIFICITY: Highest expression in brain. Also expressed in
CC parotid gland, liver, uterus, lung, heart, adrenal gland and
CC ovary. Not detected in spleen, pancreas, intestine, thymus or
CC kidney.
CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -----
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CC -----
CC EMBL; M20636; AA41885.1; -
DR PIR; A28821; A28821.
DR HSSP; P10688; 1DJX.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_Xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium.
FT DOMAIN 316 467 DOMAIN X.
FT DOMAIN 540 656 DOMAIN Y.
FT DOMAIN 663 761 C2 DOMAIN.
FT ACT_SITE 331 331 BY SIMILARITY.
FT ACT_SITE 378 378 BY SIMILARITY.
FT MOD_RES 887 887 PHOSPHORYLATION (BY PKC).
SQ SEQUENCE 1216 AA; 138344 MW; 92F23691781F788E CRC64;

Query Match 32.8%; Score 43; DB 1; Length 1216;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXKXNDNNKXK 24
DB 1059 EICEKEKELKKMKKKRQEK 1079

RESULT 10
CBF5_YEAST STANDARD; PRT; 483 AA.
AC P33322;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Centromere/microtubule binding protein CBF5 (Centromere-binding factor
DE 5) (Nucleolar protein CBF5) (P64').
GN CBF5 OR YLR175W OR L9470.11
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93330283; PubMed=8336724;
RA Jiang W., Middleton K., Yoon H.-J., Fouquet C., Carbon J.;
RT "An essential yeast protein, CBF5p, binds in vitro to centromeres and
RT microtubules.";
RL Mol. Cell. Biol. 13:4884-4893(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Entlan K.D., Floeth M., Goffeau A., Heblung U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D.,
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DR EMBL; D16824; BAA04104.1; -;  
DR HSP; P19995; IPFO.  
DR InterPro; IPR001869; Thiol\_cytolysin.  
DR Pfam; PF01289; Thiol\_cytolysin; 1.  
DR PRINTS; PR01400; FACITOLYSIN.  
DR PRODOM; PD007062; Thiol\_cytolysin; 1.  
DR PROSITE; PS00481; THIOLECYTOLYSINS; 1.  
KW Toxin; Hemolysis; Cytolysis; Signal.  
FT SIGNAL 1 36 BY SIMILARITY.  
FT CHAIN 37 574 STREPTOLYSIN O.  
FT ACT\_SITE 533 533 BINDING TO CHOLESTEROL (BY SIMILARITY).  
SQ SEQUENCE 574 AA; 63992 MW; 83345CEBDEIEBCFC CRC64;

Query Match 32.1%; Score 42; DB 1; Length 574;  
Best Local Similarity 36.4%; Pred. No. 7.4;  
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 EXXXKEXKXXDNKKKEXKXD 28  
DB 89 ESAEKEKESDNKKSEEDHTE 110

## RESULT 13

YVCE\_BACSU STANDARD; PRT; 473 AA.  
AC P40767; O06969;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical protein yvce (PSP42).  
GN YVCE.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RA Denizot F.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RN SEQUENCE OF 1-71 FROM N.A.  
RX MEDLINE=89108019; PubMed=3145906;  
RA Smith H., de Jong A., Bron S., Venema G.;  
RT "Characterization of signal-sequence-coding regions selected from the  
RL Bacillus subtilis chromosome.";  
RL Gene 70:351-361(1988).  
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C40.

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DR EMBL; Z94043; CAB08053.1; -;  
DR EMBL; Z99121; CAB15485.1; -;  
DR EMBL; M22901; AAA22817.1; ALT\_FRAME.  
DR Subtilisin; BGL1023; yvce.  
DR InterPro; IPR000064; NLPC\_P60.  
DR Pfam; PF00877; NLPC\_P60; 1.  
KW Hypothetical protein; Complete proteome.  
FT ACT\_SITE 377 377 POTENTIAL.  
SQ SEQUENCE 473 AA; 51033 MW; AF544B030E683038 CRC64;

Query Match 31.7%; Score 41.5; DB 1; Length 473;

Best Local Similarity 40.7%; Pred. No. 7.5;  
Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps 1;  
QY 7 EXXXKEXKXXDN-NKXKEXKXXDK 32  
DB 52 EAKEKEITELQENQSKIERKELKINDK 78

RESULT 14  
YMP4\_YEAST STANDARD; PRT; 519 AA.  
ID YMP4\_YEAST  
AC Q04347;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Hypothetical 60.1 kDa protein in SEC59-ERG5 intergenic region.  
GN YMR014W OR YW9711.01.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c / AB972;  
RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

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DR EMBL; Z49211; CAA89115.1; -;  
DR SGD; S0004616; YMR014W.  
KW Hypothetical protein; Coiled coil.  
FT DOMAIN 426 486 COILED COIL (POTENTIAL).  
SQ SEQUENCE 519 AA; 60054 MW; 8142768058BFA264 CRC64;

Query Match 30.5%; Score 40; DB 1; Length 519;  
Best Local Similarity 27.6%; Pred. No. 14;  
Matches 8; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXKXXDNKKKEXKXXDK 32  
DB 464 EASRSRERDRRTETNNKKEKESASTGEE 492

RESULT 15  
YPT2\_CAEEL STANDARD; PRT; 189 AA.  
ID YPT2\_CAEEL  
AC P41880;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Hypothetical 21.6 kDa protein F37A4.2 in chromosome III.  
GN F37A4.2  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Fulton L., Waterston R.;  
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.

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 CC -----

DR EMEL; U00032; AAA50630.1; -.  
 DR WormPep; F37A4.2; CE00710.

KW Hypothetical protein.

SQ SEQUENCE 189 AA; 21602 MW; 8827BCC630A015D4 CRC64;

Query Match 29.8%; Score 39; DB 1; Length 189;

Best Local Similarity 36.4%; Pred. No. 8.3;

Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Oy 7 EXXXKEXXXDNNKXKEXXD 28

Db 160 ESEKQNTVEEDKDKVEKETD 181

Search completed: June 2, 2003, 14:14:39  
 Job time : 9.32051 secs



Result No.	Query %		Length	DB	ID	Description
	Score	Match				
1	45	34.4	520	13	Q8UVZ4	O8uvz4 brachydanio
2	45	34.4	522	13	Q9DG82	Q9dg82 brachydanio
3	44	33.6	1334	5	O57322	O57322 plasmodium
4	43.5	33.2	285	13	Q9DGH7	Q9dgh7 gallus galli
5	43.5	33.2	312	13	Q9DGH8	Q9dgh8 gallus galli
6	43	32.8	1173	11	Q9Z0B5	Q9zeb5 mus musculus
7	43	32.8	1216	11	Q9Z1B3	Q9z1b3 mus musculus
8	42	32.1	52	12	O9YLS1	O9y1s1 human adeno
9	42	32.1	238	5	Q18276	Q18276 caenorhabdi
10	42	32.1	359	5	Q9V8B1	Q9v8b1 drosophila
11	42	32.1	574	2	Q9AJD4	Q9ajd4 streptococc
12	42	32.1	852	11	Q9QUG2	Q9qug2 mus musculus
13	42	32.1	965	5	O15997	O15997 bombyx mori
14	42	32.1	2285	9	O64046	O64046 bacteriopho
15	42	32.1	2285	16	O31976	O31976 bacillus su
16	41	31.3	294	5	Q95X03	Q95x03 naegleria f





FT NON\_TER 1 1  
SQ SEQUENCE 312 AA; 35275 MW; 5496BCF1B4C8676C CRC64;

Query Match 33.2%; Score 43.5; DB 13; Length 312;  
Best Local Similarity 31.2%; Pred. No. 8.7;

Matches 10; Conservative 2; Mismatches 15; Indels 5; Gaps 1;

Qy 3 CEXCEXXXKEXKXNDNNKXKEXXDXKXK 34  
||| :|||  
Db 85 CEHCESCT-----VCENGQIEKECTSTSDTVC 111

## RESULT 6

Q920E5 ID Q920E5 PRELIMINARY; PRT; 1173 AA.  
AC Q920E5;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DE Phospholipase C-beta-1B'.  
GN PLCB1 OR PLCB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SWISS 3T3;  
RA Wu K., Bai J., Marks D.L., Pagano R.E.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SWISS 3T3;  
RA Bai J., Wu K., Marks D.L., Machamer C., Pagano R.E.;  
RT "Cloning of Pi-Specific Phospholipase C's from 3T3 Cells.##I.  
RT Expression and Membrane Targeting of a Novel phospholipase C-beta-1  
RT Isoform.";  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U85714; AAD00573.1; -.  
DR EMBL; U85713; AAD00572.1; -.  
DR HSSP; P10688; LDJX.  
DR MGD; MGI:97613; Plcb1.  
DR InterPro; IPR000008; C2.  
DR InterPro; IPR001192; PI\_PLC.  
DR InterPro; IPR000909; PI\_PLC\_Xdom.  
DR InterPro; IPR001711; PI\_PLC\_Y.  
DR Pfam; PF00168; C2; 1.  
DR Pfam; PF00388; PI-PLC-X; 1.  
DR Pfam; PF00387; PI-PLC-Y; 1.  
DR PRINTS; PR00390; PHPLIPASEC.  
DR ProDom; PD001202; PI\_PLC\_Y; 1.  
DR SMART; SM00239; C2; 1.  
DR SMART; SM00148; PLCXC; 1.  
DR SMART; SM00149; PLCYC; 1.  
DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
DR PROSITE; PS50007; PIPLC\_X\_DOMAIN; 1.  
DR PROSITE; PS50008; PIPLC\_Y\_DOMAIN; 1.  
SQ SEQUENCE 1173 AA; 132255 MW; D2F5F00BE9785FFC CRC64;

Query Match 32.8%; Score 43; DB 11; Length 1173;  
Best Local Similarity 42.9%; Pred. No. 33;  
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 4 EXCEXXXKEXKXNDNNKXK 24  
||| |||  
Db 1059 EICEKEKELAKKMDKKRQEK 1079

## RESULT 7

Q921B3 ID Q921B3 PRELIMINARY; PRT; 1216 AA.  
AC Q921B3;  
DT 01-MAY-1999 (Tremblrel. 10, Created)

DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Phospholipase C-beta-1a.  
GN PLCB1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SWISS 3T3;  
RA Wu K., Bai J., Marks D.L., Pagano R.E.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U85712; AAD00571.1; -.  
DR HSSP; P10688; LDJX.  
DR MGD; MGI:97613; Plcb1.  
DR InterPro; IPR000008; C2.  
DR InterPro; IPR001192; PI\_PLC.  
DR InterPro; IPR000909; PI\_PLC\_Xdom.  
DR InterPro; IPR001711; PI\_PLC\_Y.  
DR Pfam; PF00168; C2; 1.  
DR Pfam; PF00388; PI-PLC-X; 1.  
DR Pfam; PF00387; PI-PLC-Y; 1.  
DR PRINTS; PR00390; PHPLIPASEC.  
DR ProDom; PD001202; PI\_PLC\_Y; 1.  
DR SMART; SM00239; C2; 1.  
DR SMART; SM00148; PLCXC; 1.  
DR SMART; SM00149; PLCYC; 1.  
DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
DR PROSITE; PS50007; PIPLC\_X\_DOMAIN; 1.  
DR PROSITE; PS50008; PIPLC\_Y\_DOMAIN; 1.  
SQ SEQUENCE 1216 AA; 138324 MW; D873078A58CE824D CRC64;

Query Match 32.8%; Score 43; DB 11; Length 1216;  
Best Local Similarity 42.9%; Pred. No. 34;  
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 4 EXCEXXXKEXKXNDNNKXK 24  
||| |||  
Db 1059 EICEKEKELAKKMDKKRQEK 1079

## RESULT 8

Q9YLS1 ID Q9YLS1 PRELIMINARY; PRT; 52 AA.  
AC Q9YLS1;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Hexon protein (Fragment).  
GN HEXON.  
OS Human adenovirus type 5.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=28285;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95355;  
EX MEDLINE=99143271; PubMed=9986873;  
RA Li Q.G., Henningson A., Juto P., Elgh F., Wadell G.;  
RT "Use of restriction fragment analysis and sequencing of a serotype-  
RT specific region to type adenovirus isolates.";  
RL J. Clin. Microbiol. 37:844-847(1999).  
DR EMBL; AF051949; AAD18129.1; -.  
DR HSSP; P03277; LDHX.  
DR InterPro; IPR000736; Adeno\_hexon.  
DR Pfam; PF01065; Adeno\_hexon; 1.  
DR ProDom; PD002815; Adeno\_hexon; 1.  
FT NON\_TER 1  
FT NON\_TER 52  
SQ SEQUENCE 52 AA; 5776 MW; CA787840339C61DC CRC64;

Query Match 32.1%; Score 42; DB 12; Length 52;  
Best Local Similarity 34.6%; Pred. No. 3.4;

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Matches 9; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 7 EXXXKEXXXXXNNKXKEXXDXDK 32
Db 8 ETLAKIKPAGENKWKDATERSDK 33

RESULT 9
Q18276 Q18276 PRELIMINARY; PRT; 238 AA.
AC Q18276;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 27.3 kDa protein.
DE C28C12.7.
GN C28C12.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99089613; PubMed-9851916;
RA None;
RT *Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.*;
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Miller N.;
RT *The sequence of C. elegans cosmid C28C12.*;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT *Direct Submission.*;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04079; AAB37550.2; -.
DR InterPro; IPR000004; SapB.
DR ProDom; PD001732; SapB; 1.
DR SMART; SM00118; SAPB; 4.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 27290 MW; 828BF6D21EA03866 CRC64;

Query Match 32.1%; Score 42; DB 5; Length 238;
Best Local Similarity 26.9%; Pred. No. 12;
Matches 7; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 3 CEXCXXXXKEXXXXXNNKXKEXXD 28
Db 139 CDECQFVVKELTVVDEKKSQAARD 164

RESULT 10
Q9V8B1 Q9V8B1 PRELIMINARY; PRT; 359 AA.
AC Q9V8B1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG10911 protein.
GN CG10911.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
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MedLINE-20196006; PubMed-10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Beremand B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT *The genome sequence of Drosophila melanogaster.*;
RL Science 287:2185-2195(2000).
DR EMBL; AE003801; AAF57760.1; -.
DR FLYBase; FBgn0034295; CG10911.
SQ SEQUENCE 359 AA; 37648 MW; F9B927ABC38B9215 CRC64;

Query Match 32.1%; Score 42; DB 5; Length 359;
Best Local Similarity 30.8%; Pred. No. 18;
Matches 8; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
QY 7 EXXXKEXXXXXNNKXKEXXDXDK 32
Db 76 ETASQEVQINDNTKEERDAIDASAK 101

RESULT 11
Q9AJD4 Q9AJD4 PRELIMINARY; PRT; 574 AA.
AC Q9AJD4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Streptolysin O.
GN SLO.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H46A;
RA Yamanoto I., Kimoto H., Taketo Y., Taketo A.;
RT *Mutational Analysis of Streptolysin O, an Oxygen-labile Streptococcal
RT Hemolysin.*;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050249; BAB41211.1; -;
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:43 ; Search time 11.6923 Seconds  
(without alignments)  
95.624 Million cell updates/sec

Title: US-09-780-438C-6

Perfect score: 131

Sequence: 1 XMCXCEXXXKXXKXXNNKXKEXKXXKXXKXXK 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	77.1	80	1	US-08-100-247-3
2	101	77.1	80	1	US-08-483-146A-3
3	101	77.1	80	1	US-08-232-513A-4
4	101	77.1	80	1	US-08-484-594A-3
5	101	77.1	523	1	US-08-100-247-2
6	101	77.1	523	1	US-08-483-146A-2
7	101	77.1	523	1	US-08-232-513A-3
8	101	77.1	523	1	US-08-484-594A-2
9	61	46.6	22	1	US-08-100-247-1
10	61	46.6	22	1	US-08-483-146A-1
11	61	46.6	22	1	US-08-232-513A-1
12	61	46.6	22	1	US-08-484-594A-1
13	61	46.6	22	4	US-09-231-159-1
14	61	46.6	22	4	US-08-611-307-1
15	61	46.6	22	4	US-09-148-030-1
16	56	42.7	22	4	US-09-231-159-8
17	56	42.7	22	4	US-08-611-307-8
18	54	41.2	22	1	US-08-483-146A-9
19	54	41.2	22	1	US-08-232-513A-18
20	54	41.2	22	1	US-08-484-594A-9
21	54	41.2	22	4	US-09-231-159-7
22	54	41.2	22	4	US-08-611-307-7
23	50	38.2	18	1	US-08-100-247-5
24	50	38.2	18	1	US-08-483-146A-5
25	50	38.2	18	1	US-08-232-513A-6
26	50	38.2	18	1	US-08-484-594A-5
27	50	38.2	18	4	US-09-231-159-20

28	50	38.2	18	4	US-08-611-307-20	Sequence 20, Appl
29	50	38.2	18	4	US-09-148-030-2	Sequence 2, Appl
30	45	34.4	15	4	US-09-148-030-10	Sequence 10, Appl
31	42	32.1	14	4	US-09-231-159-10	Sequence 10, Appl
32	42	32.1	14	4	US-08-611-307-10	Sequence 10, Appl
33	42	32.1	2285	4	US-09-308-375-2	Sequence 2, Appl
34	38	29.0	12	4	US-09-231-159-3	Sequence 3, Appl
35	38	29.0	12	4	US-08-611-307-3	Sequence 3, Appl
36	38	29.0	12	4	US-09-148-030-3	Sequence 3, Appl
37	38	29.0	15	4	US-09-148-030-9	Sequence 9, Appl
38	38	29.0	22	1	US-08-483-146A-8	Sequence 8, Appl
39	38	29.0	22	1	US-08-232-513A-17	Sequence 17, Appl
40	38	29.0	22	1	US-08-484-594A-8	Sequence 8, Appl
41	38	29.0	22	4	US-09-231-159-6	Sequence 6, Appl
42	38	29.0	22	4	US-08-611-307-6	Sequence 6, Appl
43	37	28.2	662	4	US-09-405-728-3	Sequence 3, Appl
44	37	28.2	846	3	US-08-885-291-55	Sequence 55, Appl
45	37	28.2	846	3	US-09-107-847-2	Sequence 2, Appl

## ALIGNMENTS

### RESULT 1

US-08-100-247-3

; Sequence 3, Application US/08100247

; Patent No. 5571787

; GENERAL INFORMATION:

; APPLICANT: O'BRIEN, JOHN S.

; APPLICANT: KISHIMOTO, YASUO

; TITLE OF INVENTION: PROSAPIN AS A NEUROTROPHIC FACTOR

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: KNOBE, MARTENS, OLSON AND BEAR

; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR

; CITY: NEWPORT BEACH

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/100,247

; FILING DATE: 19930730

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Israel, Ned A.

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER: O'Brien.002A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-235-8550

; TELEFAX: 619-235-0176

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; IMMEDIATE SOURCE:

; CLONE: SAPOSIN C

; US-08-100-247-3

Query Match 77.1%; Score 101; DB 1; Length 80;

Best Local Similarity 55.9%; Pred. No. 2.2e-10;

Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;



FILING DATE: 30-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-484-594A-3

Query Match 77.1%; Score 101; DB 1; Length 80;  
Best Local Similarity 55.9%; Pred. No. 2.2e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 3 CEXCEXXXKXXKXNNKKEKEXXDXKXCK 36  
||| || | | | | | | | | | | | | | |  
Db 5 CEVCEFLVKVTKLIDNNKTEKELDAFKMCK 38

## RESULT 5

US-08-100-247-2

Sequence 2, Application US/08100247  
Patent No. 5571787

GENERAL INFORMATION:

APPLICANT: O'BRIEN, JOHN S.

APPLICANT: KISHIMOTO, YASUO

TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR

STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR

CITY: NEWPORT BEACH

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/100,247

FILING DATE: 19930730

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Israelsen, Ned A.

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: O'BRIEN.002A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 523 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

IMMEDIATE SOURCE:

CLONE: PROSAPOSIN

US-08-100-247-2

Query Match 77.1%; Score 101; DB 1; Length 523;  
Best Local Similarity 55.9%; Pred. No. 1.4e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 3 CEXCEXXXKXXKXNNKKEKEXXDXKXCK 36  
||| || | | | | | | | | | | | | | |  
Db 314 CEVCEFLVKVTKLIDNNKTEKELDAFKMCK 347

## RESULT 6

US-08-483-146A-2

Sequence 2, Application US/08483146A

Patent No. 5696080

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

APPLICANT: Kishimoto, Yasuo

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED

TITLE OF INVENTION: THEREFROM

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Blvd. 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,146A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Israelsen, Ned A.

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: MYELOS.002DV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 523 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: N-terminal

US-08-483-146A-2

Query Match 77.1%; Score 101; DB 1; Length 523;  
Best Local Similarity 55.9%; Pred. No. 1.4e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 3 CEXCEXXXKXXKXNNKKEKEXXDXKXCK 36  
||| || | | | | | | | | | | | | | |  
Db 314 CEVCEFLVKVTKLIDNNKTEKELDAFKMCK 347

## RESULT 7

US-08-232-513A-3

Sequence 3, Application US/08232513A

Patent No. 5700909

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

US-08-100-247-2

```

RESULT 8
US-08-484-594A-2
; Sequence 2, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

```

TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
 STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
 CITY: NEWPORT BEACH  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release.#1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/08/100,247  
 APPLICATION NUMBER: 19930730  
 FILING DATE: 19930730  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Israelsen, Ned A.  
 REGISTRATION NUMBER: 29,655  
 REFERENCE/DOCKET NUMBER: OBRIEN.002A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-235-8550  
 TELEFAX: 619-235-0176  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO



ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
IMMEDIATE SOURCE:  
CLONE: 22-MER FRAGMENT  
US-08-100-247-1

Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXXXNNKXE 25  
|| || - | |||| |||  
Db 1 CEFVLKVTKLIDNNKTE 20

## RESULT 10

US-08-483-146A-1  
Sequence 1, Application US/08483146A

Patent No. 596080

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

APPLICANT: Kishimoto, Yasuo

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUTROTROPIC PEPTIDES DERIVED

TITLE OF INVENTION: THEREFROM

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Blvd. 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,146A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Israel, Ned A

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: MYELOS.002DV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: Internal

US-08-483-146A-1

Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXXXNNKXE 25  
|| || - | |||| |||  
Db 1 CEFVLKVTKLIDNNKTE 20

## RESULT 11

US-08-232-513A-1  
Sequence 1, Application US/08232513A

Patent No. 5700909

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

TITLE OF INVENTION: Prosapoin and Cytokine-Derived Peptides

TITLE OF INVENTION: as Therapeutic Agents

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,513A

FILING DATE: 21-APR-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/100,247

FILING DATE: 30-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 1643

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..22

OTHER INFORMATION: /label= SapC

US-08-232-513A-1

Query Match 46.6%; Score 61; DB 1; Length 22;

Best Local Similarity 60.0%; Pred. No. 0.00032;

Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXXXNNKXE 25

|| || - | |||| |||

Db 1 CEFVLKVTKLIDNNKTE 20

## RESULT 12

US-08-484-594A-1

Sequence 1, Application US/08484594A

Patent No. 5714459

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

APPLICANT: Kishimoto, Yasuo

TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUTROTROPIC PEPTIDES

TITLE OF INVENTION: DERIVED THEREFROM

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA: US/08/484,594A  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/100,247  
;; FILING DATE: 30-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Israel, Ned A.  
;; REGISTRATION NUMBER: 29,655  
;; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-235-8550  
;; TELEFAX: 619-235-0176  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
US-08-484-594A-1  
  
Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 6 CEXXXKEXKXNDNNKXE 25  
|| || | |||| |||  
Db 1 CEFLVKEVTKLIDNNKTE 20  
  
RESULT 13  
US-09-231-159-1  
; Sequence 1, Application US/09231159  
; Patent No. 6268347  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Protoposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/09/231,159  
; CLASSIFICATION:  
; CURRENT APPLICATION NUMBER:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-09-231-159-1  
  
Query Match 46.6%; Score 61; DB 4; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 6 CEXXXKEXKXNDNNKXE 25  
|| || | |||| |||  
Db 1 CEFLVKEVTKLIDNNKTE 20  
  
RESULT 14  
US-08-611-307-1  
; Sequence 1, Application US/08611307  
; Patent No. 6271196  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Protoposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611,307  
; FILING DATE: 05-MAR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-611-307-1  
  
Query Match 46.6%; Score 61; DB 4; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 6 CEXXXKEXKXNDNNKXE 25  
|| || | |||| |||  
Db 1 CEFLVKEVTKLIDNNKTE 20  
  
RESULT 15  
US-09-148-030-1  
; Sequence 1, Application US/09148030C  
; Patent No. 6458357  
; GENERAL INFORMATION:  
; APPLICANT: White, Michael T.  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Wright, David E.  
; TITLE OF INVENTION: RETRO-INVERSO NEUROTROPHIC AND ANALGESIC

; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: MYELOS.004CPI  
; CURRENT APPLICATION NUMBER: US/09/148.030C  
; CURRENT FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: 08/926,015  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-148-030-1

Query Match 46.6%; Score 61; DB 4; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 6 CEXXXKEXKXXDNNKXKE 25  
|| || | ||| |||  
Db 1 CEFLVKEVTKLIDNNKTEKE 20

Search completed: June 2, 2003, 14:18:24  
Job time : 13.1923 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:18 ; Search time 15.1026 Seconds  
(without alignments)  
254.692 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCEXXKXXKXXKXXNNKXKEXKXXDXKXKXX 38

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues  
Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	101	77.1	38	9	US-09-780-438A-2
2	101	77.1	40	9	US-09-780-438A-1
3	101	77.1	80	10	US-09-767-007A-3
4	101	77.1	80	10	US-09-753-126-3
5	101	77.1	209	9	US-10-043-487-340
6	101	77.1	523	10	US-09-767-007A-2
7	101	77.1	524	9	US-09-870-759-60
8	101	77.1	527	9	US-09-870-759-61
9	101	77.1	527	9	US-10-060-036-73
10	101	77.1	592	10	US-09-753-126-4
11	61	46.6	22	10	US-09-767-007A-1
12	61	46.6	22	10	US-09-957-143-1
13	54	41.2	22	10	US-09-767-007A-9
14	50	38.2	18	10	US-09-767-007A-5
15	50	38.2	15	9	US-09-957-143-2
16	45	34.4	15	9	US-10-283-819-2
17	45	34.4	15	10	US-09-802-617-2
18	42	32.1	2285	10	US-09-932-183A-2
19	39	29.8	200	10	US-09-867-550-1934

Sequence 1, Appli  
Sequence 1, Appli  
Sequence 3, Appli  
Sequence 8, Appli  
Sequence 264, App  
Sequence 42, Appl  
Sequence 3, Appli  
Sequence 11, Appl  
Sequence 166, App  
Sequence 488, App  
Sequence 47, Appl  
Sequence 134, App  
Sequence 45507, A  
Sequence 5588, Ap  
Sequence 12426, A  
Sequence 12773, A  
Sequence 13139, A  
Sequence 5207, Ap  
Sequence 2, Appli  
Sequence 214, App  
Sequence 172, App  
Sequence 2, Appli  
Sequence 32, Appl  
Sequence 1, Appli  
Sequence 5193, Ap

12 9 US-10-293-819-1  
12 10 US-09-802-617-1  
12 10 US-09-957-143-3  
22 10 US-09-767-007A-8  
238 9 US-10-153-688-264  
252 10 US-09-778-927A-42  
662 9 US-10-098-808-3  
846 9 US-10-005-691-2  
855 9 US-10-245-175-11  
248 9 US-10-097-065-166  
326 9 US-10-097-065-488  
402 10 US-09-799-777-47  
324 9 US-10-286-264-134  
69 10 US-09-864-761-45507  
182 10 US-09-815-242-5588  
188 10 US-09-815-242-12426  
188 10 US-09-815-242-12773  
203 1 US-08-781-986A-5207  
470 10 US-09-855-399-2  
751 9 US-10-114-893-214  
751 9 US-10-060-036-172  
912 9 US-09-987-482-2  
2843 8 US-08-681-219-32  
2843 9 US-09-987-482-1  
817 10 US-09-815-242-5193

## ALIGNMENTS

## RESULT 1

US-09-780-438A-2  
; Sequence 2, Application US/09780438A  
; Publication No. US20030095999A1  
; GENERAL INFORMATION:  
; APPLICANT: Cincinnati Childrens Hospital Research Foundation  
; TITLE OF INVENTION: Fusogenic Properties of Saposin C and Related Proteins and Po  
; FILE REFERENCE: 10872/0474352  
; CURRENT APPLICATION NUMBER: US/09/780,438A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,754  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-780-438A-2

Query Match 77.1% Score 101; DB 9; Length 38;  
Best Local Similarity 55.9%; Pred. No. 2.8e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 3 CEXEXKXXKXXKXXKXXKXXKXXKXXKXXK 36

Db 3 CEVCEFLVKVTKLIDNNKTEKEILDADFDMCKSK 36

## RESULT 2

US-09-780-438A-1  
; Sequence 1, Application US/09780438A  
; Publication No. US20030095999A1  
; GENERAL INFORMATION:  
; APPLICANT: Cincinnati Childrens Hospital Research Foundation  
; TITLE OF INVENTION: Fusogenic Properties of Saposin C and Related Proteins and Po  
; FILE REFERENCE: 10872/0474352  
; CURRENT APPLICATION NUMBER: US/09/780,438A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,754





<b>Qy</b>	3 CEXCEXXXKXXXXDNNXKEXXDXDKXCXK 36 
<b>Dd</b>	5 CEVCEFLVKEVTKLIDNNTKEITLDAFKMCKSK 38 

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RESULT 11
US-09-767-007A-1
; Sequence 1, Application US/09767007A
; Patent No. US20020077275A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: Yasuo Kishimoto
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS.2DCL1C1
; CURRENT APPLICATION NUMBER: US/09767,007A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial peptide
US-09-767-007A-1

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RESULT 12
US-09-957-143-1
; Sequence 1, Application US/09957143
; Patent No. US20020128193A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: David E. Wright
; TITLE OF INVENTION: RETRO-INVERSO PROSAPOSIN-DERIVED
; TITLE OF INVENTION: PEPTIDES AND USE THEREOF
; FILE REFERENCE: MYELOS 018C1
; CURRENT APPLICATION NUMBER: US/09/957,143
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: PCT/US00/08550
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/126,991
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-957-143-1

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RESULT 13
US-09-767-007A-9
; Sequence 9, Application US/09767007A
; Patent No. US2002007725A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: Yasuo Kishimoto
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SAPOGIN C AND NEUROTROPIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS.2DC1C1
; CURRENT APPLICATION NUMBER: US/09/767,007A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial peptide
US-09-767-007A-9

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RESULT 14
US-09-767-007A-5
; Sequence 5, Application US/09767007A
; Patent No. US2002007725A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: Yasuo Kishimoto
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SPSOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS.2DC1C1
; CURRENT APPLICATION NUMBER: US/09/767,007A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial peptide
US-09-767-007A-5

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RESULT 15  
US-09-957-143-2  
; Sequence 2, Application US/09957143  
; Patent No. US20020128193A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: David E. Wright



```

; TITLE OF INVENTION: RETRO-INVERSO PROSAPOSIN-DERIVED
; TITLE OF INVENTION: PEPTIDES AND USE THEREOF
; FILE REFERENCE: MYELOS.018C1
; CURRENT APPLICATION NUMBER: US/09/957,143
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: PCT/US00/08550
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/126,991
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-957-143-2

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Query Match      38.2%  Score 50;  DB 10;  Length 18;
Best Local Similarity 66.7%  Pred. No. 0.039;
Matches 10;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

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Qy      11 KEXXXDNNKXKE 25
      || | ||| |||
Db       2 KEVKLIDNNKTEKE 16

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Search completed: June 2, 2003, 14:17:53  
Job time : 15.1026 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2003, 14:15:48 ; Search time 35 Seconds.  
(without alignments)  
144.672 Million cell

**Title:** US-09-780-438C-6

Perfect score:

Sequence: 1 XXCEXCEXXXKEXXKXXXDNKXEXXDXDXDKXXCXXX 38

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

100% Processing. Minimum Match 0%  
Maximum Match 100%

Maximum Match 1008  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	131	100.0	80	16	AAW70784	Saposin-C. Homo s
2	131	100.0	80	20	AAW85653	Human saposin C.
3	131	100.0	80	22	AAU05697	Human Saponin C, S
4	131	100.0	523	22	AAW31916	Amino acid sequenc
5	131	100.0	524	16	AAW70783	Prosaposin. Homo
6	131	100.0	524	20	AAW85652	Human prosaposin N
7	131	100.0	524	21	AAV58716	Human prosaposin.
8	131	100.0	527	22	AAW31915	Amino acid sequenc
9	131	100.0	592	22	AAU05698	Human glucocerebro
10	85	64.9	25	22	AAW67289	Human saposin C.

11	77	58.8	22	16	AAE70773	Saposin-C neurotro
12	77	58.8	22	18	AAW30013	Prosaposin-derived
13	77	58.8	22	19	AAW66127	Prosaposin recepto
14	77	58.8	22	20	AAW85656	Prosaposin recepto
15	77	58.8	22	22	AAW67305	Peptide #5. Homo
16	76	58.0	21	21	AAW82281	Human saposin C 22
17	74	56.5	340	22	ABG22055	Novel human diagn
18	72	55.0	22	18	AAW30028	Mutant human prosa
19	72	55.0	22	19	AAW66134	Prosaposin derivat
20	71	54.2	25	22	ABW67293	Bovine saposin C.
21	71	54.2	744	22	ABW62390	Drosophila melanog
22	70	53.4	22	18	AAW30018	Bovine prosapoin-
23	70	53.4	22	19	AAW66133	Prosaposin recepto
24	70	53.4	22	20	AAW85661	Prosaposin recepto
25	70	53.4	554	23	ABW57102	Mouse ischaemic co
26	70	53.4	953	22	ABW58389	Drosophila melanog
27	69	52.7	567	22	AAW39351	Human polypeptide
28	69	52.7	571	22	AAW41137	Human polypeptide
29	68	51.9	2285	20	AAW98149	Bacillus subtilis
30	67	51.1	324	22	ABG05901	Novel human diagn
31	66.5	50.8	540	22	ABG59403	Drosophila melanog
32	66	50.4	459	22	ABG21310	Novel human diagn
33	66	50.4	1036	23	ABW93295	Herbicidally activ
34	65.5	50.0	666	22	ABG12052	Novel human diagn
35	65.5	50.0	1058	22	AAW80177	Human protein SEQ
36	65.5	50.0	1216	22	AAW79193	Human protein SEQ
37	65.5	50.0	1216	23	ABW08204	Human lipid metabo
38	65	49.6	578	22	ABW71910	Drosophila melanog
39	65	49.6	851	22	ABG07753	Novel human diagn
40	65	49.6	951	22	ABW97182	Human lipoprotein
41	64.5	49.2	134	22	ABE11113	Human phospholipas
42	64.5	49.2	144	21	AAW09966	Arabidopsis thalia
43	64.5	49.2	144	21	AAW50454	Arabidopsis thalia
44	64.5	49.2	159	18	AAW50288	Human Fas antigen
45	64.5	49.2	165	21	AAW03965	Arabidopsis thalia

## ALIGNMENTS

RESULT 1	
AAR70784	AAR70784 standard; Protein; 80 AA.
ID	AAR70784
XX	AC
XX	AAR70784;
XX	AC
XX	DT
XX	30-AUG-1995 (first entry)
XX	DE
XX	Saposin-C.
XX	DE
XX	XX
XX	Saposin-C; neuron; myelination; nervous system; neuroblastoma;
KW	neurotrophic peptide; multiple sclerosis; leukoencephalitis;
KW	adrenal leukodystrophy.
KW	XX
XX	XX
XX	XX
OS	Homo sapiens.
XX	XX
PN	WO9503821-A.
XX	XX
XX	09-FEB-1995.
XX	XX
XX	28-JUL-1994; 94WO-US08453.
XX	XX
XX	XX
PR	30-JUL-1993; 93US-0100247.
PR	21-APR-1994; 94US-0232513.
XX	XX
PA	(OBRI/) OBRIEN J S.
XX	XX
PI	Kishimoto Y, Obrien JS;
XX	XX
XX	WPI; 1995-082029/11.
XX	XX
PT	Stimulating neural cell out-growth and myelination - with
PT	pro: saposin, saposin C or new neurotrophic peptide(s) from

PT cytokine(s), for treating nervous system diseases

PS Disclosure; Page 32; 50pp; English.

CC The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neuroepoietic cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma.  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosapoin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.

XX Sequence 80 AA;

Query Match 100.0%; Score 131; DB 16; Length 80;  
Best Local Similarity 50.0%; Pred. No. 4.4e-05;

Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECEXXXKXXKXNDNNKXKEXXDXKXXKXXKXX 38

DB 3 VYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMKSLP 40

RESULT 2

AAW85653

ID AAW85653 standard; Peptide; 80 AA.

XX AAW85653;

DT 19-JUL-1999 (first entry)

XX Human saposin C.

KW Prosapoin; saposin; prosaptides; prosapoin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.

XX Homo sapiens.

OS

XX WO9912559-A1.

PN

PD 18-MAR-1999.

XX

PF 09-SEP-1998; 98WO-0519216.

XX

PR 04-JUN-1998; 98US-0088129.

PR 09-SEP-1997; 97US-0058352.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI O'brien JS;

XX WPI; 1999-229139/19.

DR

XX

PT Use of prosapoin receptor agonist

XX

PS Claim 7; Figure 2; 90pp; English.

XX

CC Prosapoin is a 70kDa glycoprotein which is proteolytically processed

CC to generate saposins A, B, C and D, all of which are similar to each

CC other and have a similar placement of six cysteines, a glycosylation

CC site and conserved proline residues. Prosapoin, saposin C and  
CC prosapoin derived peptides (prosaptides), have therapeutic  
CC applications in promoting recovery after toxic, traumatic, myocardial  
CC ischaemic, degenerative and inherited lesions to the peripheral and  
CC central nervous system. Prosapoin receptor agonists (PRAs)  
CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
CC members which inhibit caspases, thereby inhibiting apoptosis. An  
CC additional mechanism whereby PRAs inhibit apoptosis is by blocking  
CC activation of JNK, a proapoptotic signaling component. Within  
CC several minutes after binding to the receptor, PRAs block JNK  
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
CC activation of JNK by TNF alpha is another well known mechanism for  
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
CC apoptosis. The method can be used for inhibiting apoptosis which is  
CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. Saposin C acts as a prosapoin receptor agonist.

XX Sequence 80 AA;

Query Match 100.0%; Score 131; DB 20; Length 80;

Best Local Similarity 50.0%; Pred. No. 4.4e-05;

Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECEXXXKXXKXNDNNKXKEXXDXKXXKXXKXXKXX 38

DB 3 VYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMKSLP 40

RESULT 3

AAU05697

ID AAU05697 standard; Protein; 80 AA.

XX AAU05697;

AC

XX 24-OCT-2001 (first entry)

DT

XX Human Saponin C, SapC.

DE

XX Human; glucocerebrosidase; GCB; lysosomal storage disease;

KW Gaucher's disease; Fabry's disease; Farber's disease;

KW G\_m1 gangliosidosis; Tay-Sachs's disease; Niemann-Pick disease;

KW Shindler disease; Hunter syndrome; Sly syndrome; Hurler syndrome;

KW Scheie syndrome; Saponin C; SapC.

XX Homo sapiens.

OS

XX WO200149830-A2.

PN

XX 12-JUL-2001.

PD

XX 29-DEC-2000; 2000WO-DK00743.

PF

XX 30-DEC-1999; 99DK-0001891.

XX 02-JUN-2000; 2000DK-0000865.

PR

XX 02-JUN-2000; 2000DK-0000866.

PR

XX (MAXY-) MAXYGEN APS.

PA

XX Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;

XX

WPI; 2001-465259/50.

Improved lysosomal enzymes and lysosomal enzyme activators useful for treating Gaucher's disease -

Example 5; Page 96; 97pp; English.

The sequence represents human Saponin C (SapC), an essential co-factor for the lysosomal enzyme glucocerebrosidase, GCB. GCB is the enzyme involved in Gaucher's disease, a lysosomal storage disease. The invention relates to introducing new glycosylation sites into lysosomal enzymes/activators like GCB to improve their bioactivity. The novel polypeptides are used for the prevention and treatment of Gaucher's disease, Fabry's disease, Farber's disease, G<sub>m1</sub>-gangliosidosis, Tay-Sach's disease, Niemann-Pick disease, Shindler disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie syndromes.

Sequence 80 AA;

Query Match 100.0%; Score 131; DB 22; Length 80;  
Best Local Similarity 50.0%; Pred. No. 4.4e-05;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCCEXEXXXKXXXXNNKKEXEXXXDXDKXCXXX 38  
::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 3 VYCEVCEFLVKETKLIDNNKTEKELDADFDMCSKLP 40

RESULT 4

AAB31916 ID AAB31916 standard; Protein; 523 AA.  
XX AC AAB31916;  
XX XX  
DT 15-MAY-2001 (first entry)  
XX XX  
XX Amino acid sequence of a human protein.

Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine; ganglioside GM2 activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy.

Homo sapiens.

WO200105422-A2.

PD 25-JAN-2001.

XX 17-JUL-2000; 2000WO-FR02057.

XX PF 15-JUL-1999; 99FR-0009372.

PR PA (INMR ) BIOMERIEUX STELHYS.

XX Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;  
XX WPI; 2001-159475/16.

XX Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand -

PS Claim 1; Page 174-175; 209pp; French.

XX The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polynucleotide sequence belonging to the CC perlecan, precursor of the retinol-binding plasma protein, precursor of the CC ganglioside GM2 activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a

CC degenerative, neurological and/or auto-immune disease. The  
CC polynucleotides and polypeptides are used for diagnosis, prognosis,  
CC prevention and treatment of multiple sclerosis (in its various forms  
CC and phases). They may also be useful in cases of e.g. Alzheimer's and  
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid  
CC polyarthritis and lupus erythematosus, including use as vaccines and  
CC in gene therapy (expression of sense or antisense sequences). They can  
CC also be used to assess efficacy of potential therapeutic agents,  
CC particularly compounds that reduce or inhibit toxicity towards glial  
CC cells.

XX

SQ Sequence 523 AA;

Query Match 100.0%; Score 131; DB 22; Length 523;  
Best Local Similarity 50.0%; Pred. No. 0.00059;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCCEXEXXKEXKXXDNKNKXEKEXDXDKXCXKX 38  
:::|||||:::|||||:::|||||:::|||||:::  
Db 312 VYCEVCEFLVKETKLIDNNKTEKEILDADFDMCSKLP 349

RESULT 5

AAR70783

ID AAR70783 standard; Protein; 524 AA.

XX AC AAR70783;

XX

DT 30-AUG-1995 (first entry)

XX Prosaposin.

DE XX

KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW adrenal leukodystrophy; prosaposin.

XX

OS Homo sapiens.

XX

PN W0950382I-A.

XX

PD 09-FEB-1995.

XX

PF 28-JUL-1994; 94WO-US08453.

XX

PR 30-JUL-1993; 93US-0100247.

PR 21-APR-1994; 94US-0232513.

XX

PA (OBRI)/ OBRIEN J S.

XX

PI Kishimoto Y, Obrien JS;

XX

DR WPI: 1995-082029/11.

DR N-PSDB: AAQ85355.

XX

PT Stimulating neural cell out-growth and myelination - with  
PT pro:saposin, saposin C or new neurotrophic peptide(s) from  
PT cytokine(s), for treating nervous system diseases

XX

PS Disclosure; Page 30-32; 50pp; English.

XX

CC The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neuropoietic cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosapoin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.

XX

SQ Sequence 524 AA;

Query Match 100.0%; Score 131; DB 16; Length 524;

Best Local Similarity 50.0%; Pred. No. 0.00059;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXEXXKXKXNDNKKXKXKXDXKXKXKX 38  
DB 313 VYCEVCEFLVKEVTKLIDNKKTEKILDAFKMCSKLP 350

RESULT 6  
AAW85652  
ID AAW85652 standard; Protein; 524 AA.  
AC AAW85652;  
XX  
XX 19-JUL-1999 (first entry)  
XX Human prosaposin N-terminal peptide.  
XX  
KW Prosaposin; saposin; prosaposins; prosaposin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
XX  
XX Homo sapiens.  
XX  
XX WO9912559-A1.  
XX  
PD 18-MAR-1999.  
XX  
XX 09-SEP-1998; 98WO-US19216.  
XX  
XX 04-JUN-1998; 98US-0088129.  
XX  
XX 09-SEP-1997; 97US-0058352.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX O'brien JS;  
XX  
XX WPI; 1999-229139/19.  
XX  
XX N-PSDB; AAX08488.  
XX  
XX Use of prosaposin receptor agonist  
XX  
XX Claim 7; Figure 2; 90pp; English.  
XX  
XX Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
XX to generate saposins A, B, C and D, all of which are similar to each  
XX other and have a similar placement of six cysteines, a glycosylation  
XX site and conserved proline residues. Prosaposin, saposin C and  
XX prosaposin derived peptides (prosaposins), have therapeutic  
XX applications in promoting recovery after toxic, traumatic, myocardial  
XX ischemic, degenerative and inherited lesions to the peripheral and  
XX central nervous system. Prosaposin receptor agonists (PRAs)  
XX inhibit proinflammatory cytokine-induced apoptosis by activation of  
XX the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
XX family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
XX members which inhibit caspases, thereby inhibiting apoptosis. An  
XX additional mechanism whereby PRAs inhibit apoptosis is by blocking  
XX activation of JNK, a proapoptotic signaling component. Within  
XX several minutes after binding to the receptor, PRAs block JNK  
XX activation induced by tumor necrosis factor-alpha (TNF alpha). The  
XX activation of JNK by TNF alpha is another well known mechanism for  
XX TNF alpha-induced, as well as other proinflammatory cytokine-induced  
XX apoptosis. The method can be used for inhibiting apoptosis which is

CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. This 524 N-terminal peptide of prosaposin also acts  
CC as a prosaposin receptor agonist.  
XX  
XX SQ Sequence 524 AA;  
XX  
XX Query Match 100.0%; Score 131; DB 20; Length 524;  
XX Best Local Similarity 50.0%; Pred. No. 0.00059;  
XX Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXEXXKXKXNDNKKXKXKXDXKXKXKX 38  
DB 313 VYCEVCEFLVKEVTKLIDNKKTEKILDAFKMCSKLP 350

RESULT 7  
AAW58716  
ID AAY58716 standard; Protein; 524 AA.  
XX  
AC AAY58716;  
XX  
XX 25-APR-2000 (first entry)  
XX Human prosaposin.  
XX  
XX Prosaposin; saponin B; antiangiogenic; angiogenesis inhibitor;  
XX antitumour; antiproliferative; antimigratory; Kaposi's sarcoma;  
XX tumour; human; therapy.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT Protein /note= "mature saposin B"  
XX FT Peptide /note= "specifically claimed antiangiogenic peptide  
XX of Claim 23"  
XX FT Peptide /note= "specifically claimed antiangiogenic peptide  
XX of Claim 4"  
XX  
XX WO200002902-A1.  
XX  
XX 20-JAN-2000.  
XX  
XX 12-JUL-1999; 99WO-US15772.  
XX  
XX 13-JUL-1998; 98US-0092647.  
XX  
XX (GILL/) GILL P S.  
XX  
XX Gill PS;  
XX  
XX WPI; 2000-171128/15.  
XX  
XX Saposin B derived peptides, useful as inhibitors of angiogenesis and  
XX tumor growth -  
XX  
XX Disclosure; Page 18; 78pp; English.  
XX  
XX The present sequence is that of human prosaposin, a precursor of  
XX saposin B. The invention is based on the discovery that saposin B,  
XX previously known to be involved in the hydrolysis of sphingolipids,







XX Human; prosaposin; neural disorder; demyelination disorder;  
KW neural cell death; inhibition; myelination; neurite outgrowth;  
KW neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy;  
KW polyneuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus.  
XX  
OS Homo sapiens.  
XX  
XX WO9732895-A1.  
XX  
PN 12-SEP-1997.  
XX  
XX 05-MAR-1997; 97WO-US04143.  
XX  
XX 05-MAR-1996; 96US-0611307.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX O'Brien JS;  
XX  
XX WPI; 1997-470538/43.  
XX  
XX Prosaposin-derived peptide - useful for therapy of neural or  
PT demyelination disorders in neural tissue  
XX  
XX Claim 9; Page 52; 69pp; English.  
XX  
XX The present sequence represents a prosaposin-derived peptide. A method  
CC has been developed of alleviating or preventing neuropathic pain in a  
CC subject, comprising administering an effective amount of an active  
CC fragment of prosaposin to the subject. The prosaposin-derived peptide  
CC is useful for therapy of neural or demyelination disorders in neural  
CC tissue. It can be used to stimulate neurite outgrowth, inhibit neural  
CC cell death, promote myelination or inhibit demyelination. The method  
CC is used to alleviate neuropathic pain resulting from a peripheral nerve  
CC disorder, such as neuroma, nerve compression, crush or stretch and  
CC incomplete nerve transection, mononeuropathy or polyneuropathy.  
CC Alternatively the neuropathic pain results from a disorder of the  
CC dorsal root ganglia, spinal cord, brainstem, thalamus or cortex.  
XX  
XX Sequence 22 AA;  
XX  
Query Match 58.8%; Score 77; DB 18; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CEXXXKEXKXXDNKKEXKXX 27  
DB 1 CEFVKEVTKLIDNNKKEKIL 22  
RESULT 13  
AAW66127  
ID AAW66127 standard; peptide; 22 AA.  
XX  
AC AAW66127;  
XX  
XX 17-NOV-1998 (first entry)  
DT  
DE Prosaposin receptor agonist #1.  
XX  
XX prosaposin; receptor agonist; neuropathic pain; neurite outgrowth;  
KW neural cell death; nerve disorder; side effect.  
XX  
XX Synthetic.  
OS  
OS Homo sapiens.  
XX  
XX WO9839357-A1.  
XX  
XX 11-SEP-1998.  
XX  
XX 11-SEP-1997; 97WO-US16062.  
XX

PR 05-MAR-1997; 97WO-US04143.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX O'Brien JS;  
XX  
XX WPI; 1998-495790/42.  
DR N-PSDE; AAV07664.  
XX  
XX Use of prosaposin receptor agonists - for alleviating neuropathic  
PT pain, inhibiting sensory or motor neuropathy, or inhibiting neural  
PT cell death  
XX  
XX Claim 3; Page 2; 67pp; English.  
XX  
XX The invention relates to prosaposin receptor agonists. Also claimed  
CC are: (1) methods for alleviating neuropathic pain or inhibiting the  
CC onset of neuropathic pain, comprising administering a prosaposin receptor  
CC agonist; (2) inhibiting sensory or motor neuropathy, comprising  
CC contacting neuronal cells with a composition comprising a prosaposin  
CC receptor agonist; (3) methods for stimulating neurite outgrowth,  
CC inhibiting neural cell death, promoting myelination, or inhibiting  
CC demyelination comprising contacting neuronal cells with a composition  
CC comprising a prosaposin receptor agonist which has 14-50 amino acids and  
CC comprises the sequence of a prosaposin derived protein. The processes  
CC may be used for treatment of neuropathic pain resulting from peripheral  
CC nerve disorders (e.g. neuroma, nerve compression, nerve crush, nerve  
CC stretch, incomplete nerve transection, mononeuropathy or polyneuropathy)  
CC or disorders of dorsal root ganglia, the spinal cord, the brainstem, the  
CC thalamus or the cortex. The receptor agonists do not cause undesirable  
CC side effects. The present sequence represents a specifically claimed  
CC prosaposin receptor agonist.  
XX  
XX Sequence 22 AA;  
XX  
Query Match 58.8%; Score 77; DB 19; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CEXXXKEXKXXDNKKEXKXX 27  
DB 1 CEFVKEVTKLIDNNKKEKIL 22  
RESULT 14  
AAW85656  
ID AAW85656 standard; Peptide; 22 AA.  
XX  
AC AAW85656;  
XX  
XX 19-JUL-1999 (first entry)  
DT  
DE Prosaposin receptor agonist.  
XX  
XX Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
XX  
XX Homo sapiens.  
OS  
XX WO9912559-A1.  
XX  
XX 18-MAR-1999.  
PD

XX 09-SEP-1998; 98WO-US19216.  
XX 04-JUN-1998; 98US-0088129.  
XX 09-SEP-1997; 97US-0058352.  
XX (REGC ) UNIV CALIFORNIA.  
XX O'brien JS;  
XX WPI; 1999-229139/19.  
XX Use of prosaposin receptor agonist  
XX Claim 7; Page 66; 90pp; English.  
XX Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
XX to generate saposins A, B, C and D, all of which are similar to each  
XX other and have a similar placement of six cysteines, a glycosylation  
XX site and conserved proline residues. Prosaposin, saposin C and  
XX prosaposin derived peptides (prosapitides), have therapeutic  
XX applications in promoting recovery after toxic, traumatic, myocardial  
XX ischaemic, degenerative and inherited lesions to the peripheral and  
XX central nervous system. Prosaposin receptor agonists (PRAs)  
XX inhibit proinflammatory cytokine-induced apoptosis by activation of  
XX the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
XX family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
XX members which inhibit caspases, thereby inhibiting apoptosis. An  
XX additional mechanism whereby PRAs inhibit apoptosis is by blocking  
XX activation of JNK, a proapoptotic signaling component. Within  
XX several minutes after binding to the receptor, PRAs block JNK  
XX activation induced by tumor necrosis factor-alpha (TNF alpha). The  
XX activation of JNK by TNF alpha is another well known mechanism for  
XX TNF alpha-induced, as well as other proinflammatory cytokine-induced  
XX apoptosis. The method can be used for inhibiting apoptosis which is  
XX caspase-mediated or induced by a proinflammatory cytokine, for  
XX example TNF alpha or interferon-gamma. It can be used for inhibiting  
XX apoptosis associated with a disorder such as e.g. rheumatoid  
XX arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
XX infarction, congestive heart failure, multiple sclerosis, acute  
XX disseminated inflammatory leukoencephalitis, progressive multifocal  
XX leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
XX amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
XX disease, Guillain-Barre disease, traumatic brain injury, traumatic  
XX spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
XX neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
XX liver disease. This peptide corresponds to amino acids 8 to 29 of  
XX human saposin C (See AAW65653) and acts as a prosaposin receptor  
XX agonist.  
XX  
XX Sequence 22 AA;  
Query Match 58.8%; Score 77; DB 20; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CEXXXKEXXXKXNDNKKEXX 27  
DB 1 CEPLVREVTKLIDNNKTEKIL 22  
RESULT 15  
AAB67305  
ID AAB67305 standard; Peptide; 22 AA.  
XX  
XX AAB67305;  
XX  
XX 20-APR-2001 (first entry)  
XX Peptide #5.  
XX  
XX Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.

OS Homo sapiens.  
XX PN EP1072609-A2.  
XX 31-JAN-2001.  
XX 30-JUN-2000; 2000EP-0305504.  
XX 30-JUN-1999; 99JP-0185155.  
XX (SAKA/) SAKANAKA M.  
XX (TANA/) TANAKA J.  
XX (SATO/) SATO K.  
XX Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;  
XX WPI; 2001-204263/21.  
XX Use of prosaposin-related peptides or derivatives as cytoprotective  
XX agents, for suppressing apoptosis or apoptosis-like cell death -  
XX Disclosure; Page 28; 41pp; English.  
XX The present invention relates to use of a prosaposin-related peptide  
XX or derivative, in the production of a medicament for use in  
XX preventing or delaying cell death, or in promoting the expression  
XX of cell death supporting gene product Bcl-XL. The invention is  
XX useful for preventing the death of cells e.g. brain cells,  
XX neurons and cardiac muscle cells, in vitro or ex vivo.  
XX Sequence 22 AA;  
Query Match 58.8%; Score 77; DB 22; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CEXXXKEXXXKXNDNKKEXX 27  
DB 1 CEPLVREVTKLIDNNKTEKIL 22  
Search completed: June 2, 2003, 14:19:05  
Job time : 35 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:17:59 ; Search time 16 seconds  
(without alignments)  
228.319 Million cell updates/sec

Title: US-09-780-438c-6

Perfect score: 131

Sequence: 1 XXCEXEXXKXKXNNKXKXKXKXKXKX 38

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	100.0	527	1 SAHUP	saposin precursor
2	114	87.0	80	2 S21770	saposin-C - bovine
3	89	67.9	81	2 A32026	glucosylceramide b
4	74	56.5	439	2 T18450	hypothetical prote
5	73	55.7	314	2 T15674	hypothetical prote
6	73	55.7	554	1 A28716	saposin precursor
7	71	54.2	965	2 T00207	p109 protein - sil
8	70	53.4	557	1 JH0604	saposin precursor
9	70	53.4	572	2 T20764	hypothetical prote
10	69	52.7	570	2 T08778	hypothetical prote
11	68	51.9	483	2 S41853	centromere/microtu
12	68	51.9	2285	2 T12796	probable transglyc
13	67.5	51.5	473	2 F70031	cell wall-binding
14	67	51.1	301	2 T33068	hypothetical prote
15	67	51.1	427	2 A35859	krueppel-related p
16	67	51.1	428	2 S47096	cyanase (EC 3.4.2
17	67	51.1	474	2 T12049	variant-specific s
18	67	51.1	2664	2 T28626	upp-glucose-glycop
19	66.5	50.8	1377	2 T19214	sperm tail-specifi
20	66.5	50.8	1390	2 S51364	hypothetical prote
21	66	50.4	210	2 T28771	hypothetical prote
22	66	50.4	211	2 T25911	hypothetical prote
23	66	50.4	774	2 JC2299	cell surface glyco
24	66	50.4	1036	2 T05687	beta-galactosidase
25	66	50.4	1324	2 T01508	mismatch repair en
26	65.5	50.0	176	2 T00498	probable AP2 domai
27	65.5	50.0	913	2 T46339	hypothetical prote
28	65.5	50.0	1216	2 A28822	1-phosphatidylinos
29	65.5	50.0	1216	2 A28821	1-phosphatidylinos

30	65	49.6	217	2 S23244	hypothetical prote
31	65	49.6	321	1 BWSV4	Mov-34 protein - m
32	65	49.6	488	2 S47072	finger protein HZF
33	65	49.6	504	2 S48550	hypothetical prote
34	65	49.6	588	2 E89751	protein C33E10.5 l
35	65	49.6	743	2 A29232	101K malaria antig
36	65	49.6	3228	2 T21381	hypothetical prote
37	64.5	49.2	143	2 S41017	hypothetical prote
38	64.5	49.2	165	2 T52114	probable transcrip
39	64.5	49.2	366	2 J00513	phenylalanine dehy
40	64.5	49.2	445	2 E86440	probable chloropla
41	64.5	49.2	2013	2 C71610	probable membrane
42	64	48.9	126	2 A56857	PfEMP2/MESA protei
43	64	48.9	213	2 T46069	hypothetical prote
44	64	48.9	217	2 S43193	KSI protein - hydr
45	64	48.9	219	2 T19897	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

###### SAHUP

saposin precursor [validated] - human

N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon  
ein (SAP); sphingolipid activator protein A2; sulfate sulfate activator protein  
N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D  
C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence\_revision 17-Nov-1995 #text\_change 08-Dec-2000  
C;Accession: JX0061; A57368; A42003; B42003; C42003; A30367; S34740; S36140;  
0226; I37265; I37264

R;Nakano, T.; Sandhoff, K.; Stuenkel, J.; Christomanou, H.; Suzuki, K.

J. Biochem. 105, 152-154, 1989

A;Title: Structure of full-length cDNA coding for sulfate activator, a Co-beta-gluc  
A;Reference number: JX0061; MUID:89255151; PMID:2498298

A;Accession: JX0061

A;Molecule type: mRNA

A;Residues: 1-527 <NA>

A;Cross-references: GB:D00422; NID:g220063; PIDN:BAA00321.1; PID:g220064

A;Note: alternative splice form 1

A;Accession: A57368

A;Molecule type: mRNA

A;Residues: 1-259,263-527 <NA2>

A;Cross-references: GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59494.1; PID:g337756

A;Note: alternative splice form 2

R;Rorman, E.G.; Scheinker, V.; Grabowski, G.A.

Genomics 13, 312-318, 1992

A;Title: Structure and evolution of the human prosaposin chromosomal gene.

A;Reference number: A42003; MUID:92307663; PMID:1612590

A;Accession: A42003

A;Molecule type: DNA

A;Residues: 50-140 <ROR>

A;Cross-references: GB:M86181

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)

A;Accession: B42003

A;Molecule type: DNA

A;Residues: 185-259,263-276 <R02>

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)

A;Accession: C42003

A;Molecule type: DNA

A;Residues: 305-393 <R03>

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence

A;Accession: D42003

A;Molecule type: DNA

A;Residues: 399-487 <R04>

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence

R;Rorman, E.G.; Grabowski, G.A.

Genomics 5, 486-492, 1989

A;Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sp

A;Reference number: A30367; MUID:90129043; PMID:2515150

A;Accession: A30367

A;Molecule type: mRNA

A;Residues: 1-259,263-527 <R05>

A;Cross-references: GB:J03077; NID: g183230; PIDN:AAA52560.1; PID: g183231  
A;Note: alternative splice form 2  
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdizicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Biochem. Biophys. 304, 110-116, 1993  
A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor of ceramide sulfate  
A;Reference number: S34740; MUID: 93311991; PMID: 8323276  
A;Accession: S34740  
A;Molecule type: protein  
A;Residues: 17-24; 165-172; 180-189; 301-305 <HIR>  
R;Tyynelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M. FEBS Lett. 330, 8-12, 1993  
A;Title: Storage of saposins A and D in infantile neurofasciosclerosis.  
A;Reference number: S36140; MUID: 93380576; PMID: 8370464  
A;Accession: S36140  
A;Molecule type: protein  
A;Residues: 'XX', 62, 'X', 64-65, 'X', 67-79, 'X', 81-84 <TY>  
A;Note: saposin A  
A;Accession: S36141  
A;Molecule type: protein  
A;Residues: 'XXX', 413-414, 'X', 416-428, 'X', 430-434 <TV2>  
R;Holtzman, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K. J. Biol. Chem. 266, 7556-7560, 1991  
A;Title: Sulfate activator protein. Alternative splicing that generates three mRNAs and a precursor  
A;Reference number: S36988; MUID: 91210267; PMID: 2019586  
A;Accession: S36988  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-527 <HOL>  
A;Cross-references: EMBL:M60255; NID: g337759; PIDN:AAA36594.1; PID: g337760  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebrosulfate activator protein mutant MU-9; corresponds to alternative splicing  
A;Accession: S36989  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-259, 263-527 <HO2>  
A;Cross-references: EMBL:M60257; NID: g337764; PIDN:AAA36595.1; PID: g337765  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebrosulfate activator protein mutant MU-0; corresponds to alternative splicing  
A;Accession: S36990  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240, 'S', 242-259, 261-527 <HO3>  
A;Cross-references: EMBL:M60258; NID: g337766; PIDN:AAA36596.1; PID: g337767  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebrosulfate activator protein mutant MU-6; corresponds to alternative splicing  
R;Kondoh, K.; Hineno, T.; Sano, A.; Kakimoto, Y. Biochem. Biophys. Res. Commun. 181, 286-292, 1991  
A;Title: Isolation and characterization of prosaposin from human milk.  
A;Reference number: PS0330; MUID: 92068206; PMID: 1958198  
A;Accession: PS0330  
A;Molecule type: protein  
A;Residues: 17-24, 'X', 26 <KON>  
A;Experimental source: milk  
R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 87, 2341-2344, 1990  
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosylation defect  
A;Reference number: A35985; MUID: 90207231; PMID: 2320574  
A;Accession: A35985  
A;Molecule type: mRNA  
A;Residues: 213-221 <KRE>  
A;Cross-references: GB:M32221; NID: g337761; PIDN:AAA60303.1; PID: g337762  
A;Experimental source: lymphoblast  
A;Accession: C35985  
A;Molecule type: mRNA  
A;Residues: 213-216, 'I', 218-221 <KR>  
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; the precursor of ceramide sulfate  
R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.

Eur. J. Biochem. 192, 709-714, 1990  
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein  
A;Reference number: S13195; MUID: 91006165; PMID: 2209618  
A;Accession: S13196  
A;Molecule type: protein  
A;Residues: 195-259, 263-277 <FUE>  
R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y. Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989  
A;Title: Saposin A: second cerebroside activator protein.  
A;Reference number: A32784; MUID: 89240739; PMID: 2717620  
A;Accession: A32784  
A;Molecule type: protein  
A;Residues: 60-84; 86-107; 109-119; 125-134 <MOR>  
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L. Science 241, 1098-1101, 1988  
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same gene  
A;Reference number: A41240; MUID: 88321660; PMID: 2842863  
A;Accession: A41240  
A;Molecule type: mRNA  
A;Residues: 'GSSR', 18-259, 263-299, 'D', 301-302, 'D', 304-527 <OAB>  
A;Cross-references: GB:J03086  
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987  
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein  
A;Reference number: S02289; MUID: 88068647; PMID: 2825202  
A;Accession: S02289  
A;Status: significant sequence differences  
A;Molecule type: mRNA  
A;Cross-references: EMBL:J03015  
A;Note: this sequence corrected by A41240  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 369, 1361-1365, 1988  
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein  
A;Reference number: S02028; MUID: 89207118; PMID: 3242555  
A;Accession: S02028  
A;Molecule type: protein  
A;Residues: 195-259, 263-276 <KLE>  
R;Fuerst, W.; Machleidt, W.; Sandhoff, K. Biol. Chem. Hoppe-Seyler 369, 317-328, 1988  
A;Title: The precursor of sulfate activator protein is processed to three different products  
A;Reference number: S00813; MUID: 89000190; PMID: 3048308  
A;Accession: S00813  
A;Molecule type: protein  
A;Residues: 410-487 <FU2>  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987  
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurring A(2) activator protein  
A;Reference number: S00226; MUID: 88163077; PMID: 3442600  
A;Accession: S00226  
A;Molecule type: protein  
A;Residues: 314-393 <KL2>  
R;Vaccaro, A.M.; Salvio, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Sicilia, J. Biol. Chem. 270, 9953-9960, 1995  
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide bonds  
A;Reference number: A57297; MUID: 95247790; PMID: 7730378  
A;Contents: annotation; disulfide bonds; glycosylation  
R;Holtzman, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K. FEBS Lett. 280, 267-270, 1991  
A;Title: The organization of the gene for the human cerebroside sulfate activator protein  
A;Reference number: I37264; MUID: 91192146; PMID: 2013321  
A;Accession: I37265  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 59-125 <RES>  
A;Cross-references: EMBL:X57107; NID: g30234; PIDN:CAA40391.1; PID: g30235  
A;Accession: I37264  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 307-516 <RE2>  
A;Cross-references: EMBL:X57108; NID: g30232; PIDN:CAA40392.1; PID: g1565257  
A;Note: sequence revised relative to PID: g30233 (corrected coding region)  
C;Genetics:







hypothetical protein C35E7.9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T33068  
R:Graves, T.; McDonald, R.  
submitted to the EMBL Data Library, May 1998  
A:Description: The sequence of C. elegans cosmid C35E7.  
A:Reference number: Z21278  
A:Accession: T33068  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-301 <GRA>  
A:Cross-references: EMBL:AF067216; PIDN:AAC17524.1; GSPDB:GN00019; CESP:C35E7.9  
A:Experimental source: strain Bristol N2; clone C35E7  
C:Genetics:  
A:Gene: CESP:C35E7.9  
A:Map position: 1  
A:Introns: 30/3; 193/1; 236/2

Query Match 51.1%; Score 67; DB 2; Length 301;  
Best Local Similarity 31.2%; Pred. No. 1.6e+02;  
Matches 10; Conservative 19; Mismatches 3; Indels 0; Gaps 0;

QY 7 EXXXKEXXXNNKXEXXXDXKXKXX 38  
Db 85 KDKKEAKEDDKDKKDKKDKDDKDD 116

RESULT 15  
A35659  
krueppel-related protein H-plk - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 01-Dec-2000  
C:Accession: A35659  
R:Kato, N.; Shimotohno, K.; VanLeeuwen, D.; Cohen, M.  
Mol. Cell. Biol. 10, 4401-4405, 1990  
A:Title: Human proviral mRNAs down regulated in choriocarcinoma encode a zinc finger protein  
A:Reference number: A35659; MUID:90318410; PMID:2115127  
A:Accession: A35659  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-427 <KAT>  
A:Cross-references: GB:M55422; NID:gl84342; PIDN:AAA36010.1; PID:gl84343  
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 51.1%; Score 67; DB 2; Length 427;  
Best Local Similarity 21.1%; Pred. No. 2.1e+02;  
Matches 8; Conservative 22; Mismatches 8; Indels 0; Gaps 0;

QY 1 XXCEXEXXXKXXNNKXEXXXDXKXKXX 38  
Db 305 YKCEGKAFKQFSLTDHKKIHTGKPKYKCEGKAF 342

Search completed: June 2, 2003, 14:20:21  
Job time : 17 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2003, 14:16:28 ; Search time 11 Seconds  
(without alignments)  
143.282 Million cell updates/sec

Title: US-09-780-438c-6

Perfect score: 131

Sequence: 1 XCCEXCEXXXKXXXXNNKXKXXXXXXKXXX 38

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	100.0	524	1 SAP_HUMAN	P07602 h proactiva
2	117	89.3	525	1 SAP_BOVIN	P26779 b proactiva
3	89	67.9	81	1 SAP_CAVPO	P20097 cavia porce
4	86	65.6	518	1 SAP_CHICK	O13035 gallus gall
5	73	55.7	554	1 SAP_RAT	P10960 rattus norv
6	70	53.4	557	1 SAP_MOUSE	Q61207 mus musculu
7	70	53.4	572	1 NH25_CAEEL	Q19345 caenorhabdi
8	68	51.9	472	1 ZIM3_HUMAN	Q36966 homo sapien
9	68	51.5	483	1 CBF5_YEAST	P33322 saccharomyc
10	67.5	51.5	473	1 YVCE_BACSU	P40767 bacillus su
11	66.5	50.8	1391	1 MST2_DROHY	Q08696 drosophila
12	66	50.4	1324	1 MSH6_ARATH	O04716 arabidopsis
13	65.5	50.0	1216	1 PTBL_BOVIN	P10894 bos taurus
14	65.5	50.0	1216	1 PTBL_HUMAN	Q9nq66 homo sapien
15	65.5	50.0	1216	1 PTBL_RAT	P10687 rattus norv
16	65	49.6	180	1 YOW6_CAEEL	P30652 caenorhabdi
17	65	49.6	321	1 PSD7_MOUSE	P36516 mus musculu
18	65	49.6	488	1 Z345_HUMAN	O14585 homo sapien
19	65	49.6	504	1 STK1_YEAST	Q12460 saccharomyc
20	65	49.6	630	1 PAD5_HUMAN	Q9nqx1 homo sapien
21	65	49.6	743	1 ABRA_PLAFC	P22620 plasmodium
22	65	49.6	783	1 ZF25_HUMAN	Q9u115 homo sapien
23	64.5	49.2	366	1 DPHF_THEIN	P22823 thermoactin
24	64	48.9	217	1 K51_HYDAT	P38978 hydra atten
25	64	48.9	474	1 CBF5_KLUJA	O13473 kluyveromyc
26	64	48.9	1048	1 Z217_HUMAN	O75362 homo sapien
27	64	48.9	1451	1 AZM2_MOUSE	P28666 mus musculu
28	63.5	48.5	60	1 FER_THEMA	P46797 thermotoga
29	63.5	48.5	92	1 VF07_VACCC	P21016 vaccinia vi
30	63	48.1	238	1 NEUM_HUMAN	P17677 homo sapien
31	63	48.1	473	1 CYP1_CYNCA	P40782 cynara card
32	63	48.1	474	1 Z141_HUMAN	Q35928 homo sapien
33	63	48.1	479	1 CBF5_CANAL	Q43101 candida alb

#### RESULT 1

ID	SAP_HUMAN	STANDARD;	PRT;	524 AA.
AC	P07602; P07292; P15793; P78538; P78546; P78547; Q92741; Q92742;			
AC	Q92740; Q92739; P78541; P78558;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Proactivator polypeptide precursor [Contains: Saposin A (Protein A);			
DE	Sapostin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside			
DE	sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator);			
DE	Sapostin C (Co-beta-glucosidase) (AI activator) (Glucosylceramidase			
DE	activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D			
DE	(Protein C) (Component C)].			
GN	PSAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Liver;			
RC	MEDLINE=90129043; PubMed=2515150;			
RA	Roman E.G., Grabowski G.A.;			
RT	"Molecular cloning of a human co-beta-glucosidase cDNA: evidence that			
RT	four sphingolipid hydrolase activator proteins are encoded by single			
RT	genes in humans and rats.";			
RL	Genomics 5:486-492(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=89255151; PubMed=2498298;			
RA	Nakano T., Sandhoff K., Stuenkel J., Christomanou H., Suzuki K.;			
RT	"Structure of full-length cDNA coding for sulfatide activator, a			
RT	Co-beta-glucosidase and two other homologous proteins: two alternate			
RT	forms of the sulfatide activator.";			
RL	J. Biochem. 105:152-154(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye, and Skin;			
RA	Strausberg R.;			
RT	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 59-125 AND 304-513 FROM N.A.			
RC	TISSUE=Brain;			
RA	MEDLINE=91192146; PubMed=2013321;			
RA	Holtschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D.,			
RA	Suzuki K.;			
RT	"The organization of the gene for the human cerebroside sulfate			
RT	activator protein.";			
RL	FEBS Lett. 280:267-270(1991).			
RN	[5]			
RP	SEQUENCE OF 164-524 FROM N.A.			
RA	MEDLINE=88068647; PubMed=2825202;			
RA	Dewji N.N., Wenger D.A., O'Brien J.S.;			
RT	"Nucleotide sequence of cloned cDNA for human sphingolipid activator			
RT	protein 1 precursor.";			

P42210 hordeum vul  
P16374 mus musculu  
Q9ju3 homo sapien  
P10251 mycoplasma  
Q04347 saccharomyc  
Q53957 streptococc  
Q54114 streptococc  
Q9uk13 homo sapien  
P13816 plasmodium  
P39055 caenorhabdi  
P13828 plasmodium  
Q15911 homo sapien

#### ALIGNMENTS

RA Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).  
[6]  
RP PARTIAL SEQUENCE OF 60-142.  
RX MEDLINE-89240739; PubMed-2717620;  
RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,  
RA Kishimoto Y.;  
RT "Saposin A: second cerebroside activator protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).  
[7]  
RP SEQUENCE OF 195-263 FROM N.A.  
RX MEDLINE-86130593; PubMed-2858718;  
RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,  
RA Hill F., O'Brien J.S.;  
RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),  
RT the sulfatide sulfatase activator.";  
RL Biochem. Biophys. Res. Commun. 134:989-994(1986).  
[8]  
RP SEQUENCE OF 195-274.  
RX TISSUE=Urine;  
RA MEDLINE-91006165; PubMed-2209618;  
RT Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;  
RT "The complete amino-acid sequences of human ganglioside GM2 activator  
RT protein and cerebroside sulfate activator protein.";  
RL Eur. J. Biochem. 192:709-714(1990).  
[9]  
RP SEQUENCE OF 195-274.  
RX MEDLINE-89207118; PubMed-3242555;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence of the naturally occurring A2 activator  
RT protein for enzymic sphingomyelin degradation: identity to the  
RT sulfatide activator protein (SAP-1).";  
RL Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).  
[10]  
RP SEQUENCE OF 311-390.  
RX MEDLINE-88163077; PubMed-3442600;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence and carbohydrate content of the  
RT naturally occurring glucosylceramide activator protein (A1 activator)  
RT absent from a new human Gaucher disease variant.";  
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).  
[11]  
RP SEQUENCE OF 407-484.  
RX MEDLINE-89000190; PubMed-3048308;  
RA Furst W., Machleidt W., Sandhoff K.;  
RT "The precursor of sulfatide activator protein is processed to three  
RT different proteins.";  
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).  
[12]  
RP PARTIAL SEQUENCE OF 405-484.  
RX MEDLINE-89025876; PubMed-2845979;  
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;  
RT "Saposin D: a sphingomyelinase activator.";  
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).  
[13]  
RP SEQUENCE OF 17-26.  
RX TISSUE=Milk;  
RA MEDLINE-92068206; PubMed-1958198;  
RA Kondoh K., Hinenio T., Sano A., Kakimoto Y.;  
RT "Isolation and characterization of prosaposin from human milk.";  
RL Biochem. Biophys. Res. Commun. 181:286-292(1991).  
[14]  
RP PARTIAL SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.  
RX TISSUE=Urine;  
RA MEDLINE-20032116; PubMed-10562467;  
RA Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.,  
RA Waring A.J., To T., Fluharty C.B., Paull K.F.;  
RT "Preparation of the cerebroside sulfate activator (CSAct or saposin B)  
RT from human urine.";  
RL Mol. Genet. Metab. 68:391-403(1999).  
[15]  
RP STRUCTURE OF CARBOHYDRATE ON ASN-215.  
RX MEDLINE-21110404; PubMed-11180632;  
RA Paull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,

RA Stevens R.L., Fluharty C.B., Fluharty A.L.;  
RT "Structure of the asparagine-linked sugar chains of porcine kidney and  
RT human urine cerebroside sulfate activator protein.";  
RL J. Mass Spectrom. 35:1416-1424(2000).  
[16]  
RP MASS SPECTROMETRY.  
RX TISSUE=Urine;  
RA MEDLINE-99441404; PubMed-10510427;  
RA Paull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,  
RA Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,  
RA Fluharty C.B., Fluharty A.L.;  
RT "Cerebroside sulfate activator protein (Saposin B): chromatographic  
RT and electrospray mass spectrometric properties.";  
RL J. Mass Spectrom. 34:1040-1054(1999).  
[17]  
RP VARIANT MLD ILE-217.  
RX MEDLINE-90147748; PubMed-2302219;  
RA Rafi M.A., Zhang X.-L., Degala G., Wenger D.A.;  
RT "Detection of a point mutation in sphingolipid activator protein-1  
RT mRNA in patients with a variant form of metachromatic  
RT leukodystrophy.";  
RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).  
[18]  
RP SEQUENCE FROM N.A., AND VARIANT MLD ILE-217.  
RX MEDLINE-90207231; PubMed-2320574;  
RA Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluharty A.L.,  
RA O'Brien J.S.;  
RT "Characterization of a mutation in a family with saposin B  
RT deficiency: a glycosylation site defect.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).  
[19]  
RP VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE-91210267; PubMed-2019586;  
RA Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,  
RA Suzuki K.;  
RT "Sulfatide activator protein. Alternative splicing that generates  
RT three mRNAs and a newly found mutation responsible for a clinical  
RT disease.";  
RL J. Biol. Chem. 266:7556-7560(1991).  
[20]  
RP VARIANT GAUCHER PHE-388.  
RX MEDLINE-91285107; PubMed-2060627;  
RA Schnabel D., Schroeder M., Sandhoff K.;  
RT "Mutation in the sphingolipid activator protein 2 in a patient with a  
RT variant of Gaucher disease.";  
RL FEBS Lett. 284:57-59(1991).  
[21]  
RP REVIEW ON MLD VARIANTS.  
RX MEDLINE-95170731; PubMed-7866401;  
RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;  
RT "Molecular genetics of metachromatic leukodystrophy.";  
RL Hum. Mutat. 4:233-242(1994).  
CC -1- FUNCTION: The lysosomal degradation of sphingolipids takes place  
CC by the sequential action of specific hydrolases. Some of these  
CC enzymes require specific low-molecular mass, non-enzymic proteins:  
CC the sphingolipids activator proteins (coproteins).  
CC -1- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of  
CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and  
CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).  
CC Saposin C apparently acts by combining with the enzyme and acidic  
CC lipid to form an activated complex, rather than by solubilizing  
CC the substrate.  
CC -1- FUNCTION: Saposin B stimulates the hydrolysis of galacto-  
CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1  
CC gangliosides by beta-galactosidase (EC 3.2.1.23) and  
CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).  
CC Saposin B forms a solubilizing complex with the substrates of the  
CC sphingolipid hydrolases.  
CC -1- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase  
CC activator (EC 3.1.4.12).  
CC -1- SUBUNIT: Saposin B is a homodimer.  
CC -1- SUBCELLULAR LOCATION: Lysosomal.  
CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),

```
Query Match      100.0%; Score 131; DB 1; Length 524;
Best Local Similarity 50.0%; Pred. No. 0.00037;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXCEXXKEXKXXDNKKKEXKXXDKXXKXXKXX 38
    :||:||||:||||:||||:||||:||||:||||:||||:
Db 313 YICEVCEFLVKEVTKLIDNNKTEKEILDAFDKMSKLP 350

RESULT 2
SAP_BOVIN
ID SAP_BOVIN STANDARD; PRT; 525 AA.
AC P26779; Q9N2G4;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Proactivator polypeptide precursor (Contains: Saposin A (Protein A);
DE Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside
DE sulfate activator) (CSAct) (Dispersin) (Sulfatide/GMI activator);
DE Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase
DE activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
DE (Protein C) (Component C)).
GN PSAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS.
RC TISSUE-Mammary gland;
RA Azuma N., Yoshida K.;
RT "RT-PCR cloning of bovine prosaposin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 312-391.
RC TISSUE-Spleen;
RX MEDLINE=92207994; PubMed=1554743;
RA Sano A., Mizuno T., Kondoh K., Hinenio T., Ueno S.-I., Kakimoto Y.,
RA Morita N.;
RT "Saposin-C from bovine spleen: complete amino acid sequence and
RT relation between the structure and its biological activity.";
RL Blochm. Biophys. Acta 1120:75-80(1992).
CC -!- FUNCTION: THE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
CC BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
CC ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:
CC THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).
CC -!- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
CC GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND
CC GALACTOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.46).
CC SAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
CC LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
CC THE SUBSTRATE.
CC -!- FUNCTION: SAPOSIN B STIMULATES THE HYDROLYSIS OF GALACTO-
CC CEREBROSIDE SULFENE BY ARYL SULFATASE A (EC 3.1.6.8), GMI
CC GANGLIOSIDES BY BETA-GALACTOSIDASE (EC 3.2.1.23) AND
CC GLOBOTRIOSYLCERAMIDE BY ALPHA-GALACTOSIDASE A (EC 3.2.1.22).
CC SAPOSIN B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE
CC SPHINGOLIPID HYDROLASES (BY SIMILARITY).
CC -!- FUNCTION: SAPOSIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE
CC ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).
CC -!- SUBUNIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- PTM: THIS PRECURSOR IS PROTEOLYTICALLY PROCESSED TO 4 SMALL
CC PEPTIDES, WHICH ARE SIMILAR TO EACH OTHER AND ARE SPHINGOLIPID
CC HYDROLASE ACTIVATOR PROTEINS (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
-----
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CC EMBL; AB036791; BAA95677.1; -
CC PIR; S21770; S21770.
CC InterPro; IPR003119; Sapa.
CC InterPro; IPR000004; SapB.
CC Pfam; PF02199; SAPA; 2.
CC ProDom; PD001732; SapB; 4.
CC SMART; SM00162; SAPA; 2.
CC SMART; SM00118; SAPB; 4.
KW SIGNAL; Glycoprotein; Lysosome; Sphingolipid metabolism; Repeat.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 60 142 SAPOSIN A.
FT CHAIN 196 275 SAPOSIN B.
FT CHAIN 312 392 SAPOSIN C.
FT CHAIN 406 487 SAPOSIN D.
FT DOMAIN 21 54 SAPOSIN-LIKE TYPE A 1.
FT DOMAIN 59 142 SAPOSIN-LIKE TYPE B 1.
FT DOMAIN 194 276 SAPOSIN-LIKE TYPE B 2.
FT DOMAIN 312 393 SAPOSIN-LIKE TYPE B 3.
FT DOMAIN 406 487 SAPOSIN-LIKE TYPE B 4.
FT DOMAIN 492 525 SAPOSIN-LIKE TYPE A 2.
FT DISULFID 63 138 BY SIMILARITY.
FT DISULFID 66 132 BY SIMILARITY.
FT DISULFID 94 106 BY SIMILARITY.
FT DISULFID 199 272 BY SIMILARITY.
FT DISULFID 202 266 BY SIMILARITY.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 316 389 BY SIMILARITY.
FT DISULFID 319 383 BY SIMILARITY.
FT DISULFID 347 358 BY SIMILARITY.
FT DISULFID 410 483 BY SIMILARITY.
FT DISULFID 413 477 BY SIMILARITY.
FT DISULFID 441 452 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 427 427 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 127 127 H -> R.
FT VARIANT 260 263 MQPK -> IRIR.
FT CONFLICT 317 317 E -> Q (IN REF. 2).
FT CONFLICT 367 367 R -> S (IN REF. 1).
SQ SEQUENCE 525 AA; 58120 MW; 293AFC0FB9C4FA99 CRC64;

Query Match      89.3%; Score 117; DB 1; Length 525;
Best Local Similarity 42.1%; Pred. No. 0.006;
Matches 16; Conservative 21; Mismatches 1; Indels 0; Gaps

QY 1 XXCEXCEXXKEXKXXDNKKKEXKXXDKXXKXXKXX 38
    :||:||||:||||:||||:||||:||||:||||:||||:
Db 314 YICEVCEFLVKEVTKLIDNNKTEKEILDAFDKMSKLP 351

RESULT 3
SAP_CAVPO
ID SAP_CAVPO STANDARD; PRT; 81 AA.
AC P20097;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Saposin C (CO-beta-glucosidase) (Glucosylceramidase activator)
DE (Sphingolipid activator protein 2) (SAP-2).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE-Liver;
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FT REPEAT 446 448 5.
FT REPEAT 449 451 6.
FT REPEAT 452 454 7.
FT REPEAT 455 457 8.
FT REPEAT 458 460 9.
FT REPEAT 461 463 10.
SQ SEQUENCE 483 AA; 54704 MW; D356B39FDCC32E2D CRC64;

Query Match 51.9%; Score 68; DB 1; Length 483;
Best Local Similarity 32.3%; Pred. No. 94;
Matches 10; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

Qy 8 XXXKEXXXNNKXKEXXXDXKXCXXX 38
Db 422 ETEKEEVKEDSKKKEKKKKKKKKKK 452

RESULT 10
YVCE_BACSU STANDARD; PRT; 473 AA.
AC P40767; O06969;
DT 01-FEB-1995 (Rel. 31, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yvce (PSPA2).
OS Bacillus subtilis.
GN Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RA Denizot F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=69108019; PubMed=3145906;
RA Smith H., Ge Jong A., Bron S., Venema G.;
RT "Characterization of signal-sequence-coding regions selected from the
RL Bacillus subtilis chromosome.";
Gene 70:351-361(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C40.
CC -----
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CC -----
DR EMBL; Z94043; CAB08053.1; -
DR EMBL; Z99121; CAB15485.1; -
DR EMBL; M22901; AAA22817.1; ALT_FRAME.
DR Subtilisin; BG11023; YVCE.
DR InterPro; IPR000064; NLPC_P60.
DR Pfam; PF00877; NLPC_P60; 1.
KW Hypothetical protein; Complete proteome.
FT ACT_SITE 377 377 POTENTIAL.
SQ SEQUENCE 473 AA; 51033 MW; AF544B030E683038 CRC64;

Query Match 51.5%; Score 67.5; DB 1; Length 473;
Best Local Similarity 28.2%; Pred. No. 1e+02;
Matches 11; Conservative 22; Mismatches 5; Indels 1; Gaps 1;

Qy 1 XXCXCXXXKXKXNDN-NKXKEXXXDXKXCXXX 38
Db 46 EVASSTEAKEKTELQENQSKTEKELKINDKALDTSN 84

RESULT 11
MST2_DROHY STANDARD; PRT; 1391 AA.
ID MST2_DROHY

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AC Q08696;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Axoneme-associated protein mst101(2).
GN MST101(2).
OS Drosophila hydei (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7224;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=95045538; PubMed=7957199;
RA Neesen J., Padmanabhan S., Buenemann H.;
RT "Randomly arranged repeats of a novel highly charged 16-amino-acid
RT motif representing the major component of the sperm-tail-specific
RT axoneme-associated protein family Dhmst101 form extended
RT alpha-helical rods within the extremely elongated spermatozoa of
RT Drosophila hydei.";
RL Eur. J. Biochem. 225:1089-1095(1994).
CC -1- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
CC SPERMATIDS.
CC -1- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
CC -1- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
CC STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
CC REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X73481; CAA51876.1; -
DR PIR; S34154; S34154.
DR FlyBase; FBgn0020733; Dhyd\mst101(2).
KW Sperm; Repeat; Multigene family; Polymorphism.
FT DOMAIN 332 1268
[KKR]-K-X-C-X-X-A-X-K-X-X-K-X-X-X-E.
SQ SEQUENCE 1391 AA; 159000 MW; 1B2A368F30F48878 CRC64;

Query Match 50.8%; Score 66.5; DB 1; Length 1391;
Best Local Similarity 25.7%; Pred. No. 3.7e+02;
Matches 9; Conservative 23; Mismatches 2; Indels 1; Gaps 1;

Qy 4 EXCEXXXKXKXNDNKKKEXKXKXKXKXKX 38
Db 939 KKCKKLAKKKEKKEKKNLKKAG-KGKKKKKLG 972

RESULT 12
MSH6_ARATH STANDARD; PRT; 1324 AA.
ID MSH6_ARATH
AC O04716;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA mismatch repair protein MSH6-1 (AtMsh6-1).
GN MSH6-1 OR AGAA.3 OR AT4G02070 OR T10M13.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RA Till S., Granat S., Parnell L., Kaplan N., Hoffman J., Lodhi M.,

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Mon Jun 2 14:58:27 2003

us-09-780-438c-6.dx.rsp

Page 12

Search completed: June 2, 2003, 14:19:23  
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:17:24 ; Search time 29 seconds  
(without alignments)  
269.993 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCEXEXXXKXXKXXDNNKXEXXDXKXXCXXKXX 38

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	78	59.5	1334	5	O97322	O97322 plasmodium
2	74	56.5	520	13	O8UVZ4	O8UVZ4 brachydanio
3	74	56.5	522	13	O9DG82	O9DG82 brachydanio
4	74	56.5	594	5	O77337	O77337 plasmodium
5	73	55.7	238	5	O18276	O18276 caenorhabdi
6	73	55.7	294	5	O95X03	O95X03 naegleria f
7	73	55.7	307	5	O9BKW2	O9BKW2 naegleria f
8	71.5	54.6	540	16	O8XHG9	O8XHG9 clostridium
9	71	54.2	85	10	O8WIM2	O8WIM2 solanum cha
10	71	54.2	257	3	O01803	O01803 pneumocysti
11	71	54.2	744	5	O9VD23	O9VD23 drosophila
12	71	54.2	965	5	O15997	O15997 bombyx mori
13	70	53.4	231	2	O93EJ8	O93EJ8 francisella
14	70	53.4	257	5	O9NS57	O9NS57 caenorhabdi
15	70	53.4	441	5	O9U9P3	O9U9P3 drosophila
16	70	53.4	953	5	O9Y125	O9Y125 drosophila

17	69.5	53.1	285	13	O9DGH7	O9dgh7 gallus gall
18	69.5	53.1	312	13	O9DGH8	O9dgh8 gallus gall
19	69	52.7	397	4	O9BT47	O9bt47 homo sapien
20	69	52.7	444	4	O60405	O60405 homo sapien
21	69	52.7	496	4	O75760	O75760 homo sapien
22	69	52.7	567	4	O9H624	O9h624 homo sapien
23	69	52.7	570	4	O9UG74	O9ug74 homo sapien
24	69	52.7	1065	3	O01828	O01828 pneumocysti
25	68.5	52.3	1092	3	O9UVY2	O9uvy2 pneumocysti
26	68	51.9	359	5	O97326	O97326 plasmodium
27	68	51.9	1000	3	O96VI9	O96vi9 pneumocysti
28	68	51.9	2285	9	O64046	O64046 bacterioph
29	68	51.9	2285	16	O31976	O31976 bacillus su
30	67	51.1	204	5	O9N528	O9n528 caenorhabdi
31	67	51.1	301	5	O61765	O61765 caenorhabdi
32	67	51.1	304	5	O8WT00	O8wt00 plasmodium
33	67	51.1	427	4	O02313	O02313 homo sapien
34	67	51.1	568	4	O8TD23	O8td23 homo sapien
35	67	51.1	1618	11	O9QX19	O9qxi19 rattus norv
36	67	51.1	2081	10	O9LH98	O9lh98 arabidopsis
37	67	51.1	2664	5	O26033	O26033 plasmodium
38	66.5	50.8	516	5	O9Y155	O9y155 drosophila
39	66.5	50.8	540	5	O9W0X8	O9w0x8 drosophila
40	66.5	50.8	1377	5	P91854	P91854 caenorhabdi
41	66	50.4	185	5	O9Y0V9	O9y0v9 drosophila
42	66	50.4	185	5	O8SYA0	O8sya0 drosophila
43	66	50.4	210	5	O02124	O02124 caenorhabdi
44	66	50.4	211	5	P91488	P91488 caenorhabdi
45	66	50.4	296	5	O95UP8	O95up8 dictyostelli

ALIGNMENTS

RESULT 1

O97322 PRELIMINARY; PRT; 1334 AA.  
ID O97322  
AC O97322;  
DC 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Hypothetical 160.8 kDa protein.  
GN PFC1010W, MAL3P7.32.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3D7;  
RX MEDLINE=99375085; PubMed=10448855;  
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T., Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutter S., Skellon J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;  
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum";  
RL Nature 400:532-538(1999).  
DR EMBL; AL034559; CAB39073.2;  
KW Hypothetical protein.  
SQ SEQUENCE 1334 AA; 160847 MW; E3577E84C7E0C8E5 CRC64;

Query Match 59.5%; Score 78; DB 5; Length 1334;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
Matches 10; Conservative 23; Mismatches 5; Indels 0; Gaps 0;

Oy 1 XXCEXEXXXKXXKXXDNNKXEXXDXKXXCXXKXX 38  
DB 881 RKLQNLDMKKKKYENNNNNNNKDKKDKNNCKLKL 918













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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:18:29 ; Search time 15 seconds  
(without alignments)  
74.538 Million cell updates/sec

Title: US-09-780-438C-6

Perfect score: 131

Sequence: 1 XCCEXCEXXXKXXKXXNNKXKEXKXXKXXKXXKXX 38

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	100.0	80	1 US-08-100-247-3	Sequence 3, Appl
2	131	100.0	80	1 US-08-483-146A-3	Sequence 3, Appl
3	131	100.0	80	1 US-08-232-513A-4	Sequence 4, Appl
4	131	100.0	80	1 US-08-484-594A-3	Sequence 3, Appl
5	131	100.0	523	1 US-08-100-247-2	Sequence 2, Appl
6	131	100.0	523	1 US-08-483-146A-2	Sequence 2, Appl
7	131	100.0	523	1 US-08-232-513A-3	Sequence 3, Appl
8	131	100.0	523	1 US-08-484-594A-2	Sequence 2, Appl
9	77	58.8	22	1 US-08-100-247-1	Sequence 1, Appl
10	77	58.8	22	1 US-08-483-146A-1	Sequence 1, Appl
11	77	58.8	22	1 US-08-232-513A-1	Sequence 1, Appl
12	77	58.8	22	1 US-08-484-594A-1	Sequence 1, Appl
13	77	58.8	22	4 US-09-231-159-1	Sequence 1, Appl
14	77	58.8	22	4 US-08-611-307-1	Sequence 1, Appl
15	77	58.8	22	4 US-09-148-030-1	Sequence 1, Appl
16	72	55.0	22	4 US-09-231-159-8	Sequence 8, Appl
17	72	55.0	22	4 US-08-611-307-8	Sequence 8, Appl
18	70	53.4	22	1 US-08-483-146A-9	Sequence 9, Appl
19	70	53.4	22	1 US-08-232-513A-18	Sequence 18, Appl
20	70	53.4	22	1 US-08-484-594A-9	Sequence 9, Appl
21	70	53.4	22	4 US-09-231-159-7	Sequence 7, Appl
22	70	53.4	22	4 US-08-611-307-7	Sequence 7, Appl
23	68	51.9	2285	4 US-09-308-375-2	Sequence 2, Appl
24	64.5	49.2	143	4 US-09-180-100-10	Sequence 10, Appl
25	64.5	49.2	159	4 US-09-180-100-23	Sequence 23, Appl
26	64.5	49.2	360	4 US-09-180-100-11	Sequence 11, Appl
27	64.5	49.2	376	4 US-09-180-100-22	Sequence 22, Appl

28	63.5	48.5	314	1	US-08-444-231-19	Sequence 19, Appl
29	63.5	48.5	314	1	US-08-152-443A-19	Sequence 19, Appl
30	63.5	48.5	314	5	PCT-US95-17083-4	Sequence 4, Appl
31	62	47.3	514	4	US-08-796-899-25	Sequence 25, Appl
32	62	47.3	708	4	US-08-235-836C-76	Sequence 76, Appl
33	61	46.6	18	1	US-08-100-247-5	Sequence 5, Appl
34	61	46.6	18	1	US-08-483-146A-5	Sequence 5, Appl
35	61	46.6	18	1	US-08-232-513A-6	Sequence 5, Appl
36	61	46.6	18	1	US-08-484-594A-5	Sequence 5, Appl
37	61	46.6	18	4	US-09-231-159-20	Sequence 20, Appl
38	61	46.6	18	4	US-08-611-307-20	Sequence 20, Appl
39	61	46.6	18	4	US-09-148-030-2	Sequence 2, Appl
40	61	46.6	445	4	US-08-845-258-38	Sequence 38, Appl
41	61	46.6	445	4	US-08-990-571-38	Sequence 38, Appl
42	61	46.6	445	4	US-08-723-142A-38	Sequence 38, Appl
43	61	46.6	445	4	US-09-528-784A-38	Sequence 38, Appl
44	61	46.6	666	4	US-09-528-784A-85	Sequence 85, Appl
45	61	46.6	727	2	US-08-475-844-9	Sequence 9, Appl

#### ALIGNMENTS

RESULT 1  
US-08-100-247-3  
; Sequence 3, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; APPLICANT: KISHIMOTO, YASUO  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
; CITY: NEWPORT BEACH  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/100,247  
; FILING DATE: 19930730  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: OBRIEN.002A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; IMMEDIATE SOURCE:  
; CLONE: SAPOSIN C  
; US-08-100-247-3

Query Match 100.0%; Score 131; DB 1; Length 80;  
Best Local Similarity 50.0%; Pred. No. 1.6e-05;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;



FILING DATE: 30-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Israelsen, Ned A  
 REGISTRATION NUMBER: 29,655  
 REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-235-8550  
 TELEFAX: 619-235-0176  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 80 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-484-594A-3

Query Match 100.0%; Score 131; DB 1; Length 80;  
Best Local Similarity 50.0%; Pred. No. 1.6e-05;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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RESULT 5
US-08-100-247-2
; Sequence 2, Application US/08100247
; Patent No. 5571787
; GENERAL INFORMATION:
; APPLICANT: O'BRIEN, JOHN S.
; APPLICANT: KISHIMOTO, YASUO
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0; Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,247
; FILING DATE: 19930730
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: O'Brien.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: PROSAPOSIN
; US-08-100-247-2

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Query Match      100.0%; Score 131; DB 1; Length 523;
Best Local Similarity 50.0%; Pred. NO. 0.00018;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6  
 US-08-483-146A-2  
 ; Sequence 2, Application US/08483146A  
 ; Patent No. 5696080  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'Brien, John S.  
 ; APPLICANT: Kishimoto, Yasuo  
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
 ; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED  
 ; TITLE OF INVENTION: THEREFROM  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear  
 ; STREET: 620 Newport Center Blvd. 16th Floor  
 ; CITY: Newport Beach  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/483,146A  
 ; FILING DATE: 07-JUN-1995

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Query Match      100.0%; Score 131; DB 1; Length 523;
Best Local Similarity 50.0%; Pred. No. 0.00018;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	XXCECXXXXXKXXXDNKKYEKEXDXXDKXCXXX	38
		: : : : : : : : : : : : : : : : : :	
Db	312	VYCECFVKEVTKLIDNNKKEIILDAFDKWCskLP	349

RESULT 7  
US-08-232-513A-3  
; Sequence 3, Application US/08232513A  
; Patent No. 5700909  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.

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1  RESULT 8
2  US-08-484-594A-2
3  ; Sequence 2, Application US/08484594A
4  ; Patent No. 5714459
5  ; GENERAL INFORMATION:
6  ; APPLICANT: O'Brien, John S.
7  ; APPLICANT: Kishimoto, Yasuo
8  ; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPIC PEPTIDES
9  ; TITLE OF INVENTION: DERIVED THEREFROM
10 ; NUMBER OF SEQUENCES: 11
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Knobbe, Martens, Olson and Bear
13 ; SYREET: 620 Newport Center Drive, Sixteenth Floor
14 ; CITY: Newport Beach
15 ; STATE: CA
16 ; COUNTRY: USA
17 ; ZIP: 92660
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Diskette
20 ; COMPUTER: IBM Compatible
21 ; OPERATING SYSTEM: DOS
22 ; SOFTWARE: Fastseq for Windows Version 2.0
23 ; CURRENT APPLICATION DATA:

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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100,247  
FILING DATE: 19930730  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Israel, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: OBRIEN, 002A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8850  
TELEFAX: 619-235-0176  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; CLONE: 22-MER FRAGMENT
US-08-100-247-1
Query Match 58.8%; Score 77; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 0.3;
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXKEXX 27
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Db 1 CEFVKEVTKLIDNNKTEKIL 22

RESULT 10
US-08-483-146A-1
; Sequence 1, Application US/08483146A
; Patent No. 5696080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPIC PEPTIDES DERIVED
; FROM THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-483-146A-1
Query Match 58.8%; Score 77; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 0.3;
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXKEXX 27
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Db 1 CEFVKEVTKLIDNNKTEKIL 22

RESULT 11
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US-08-232-513A-1
; Sequence 1, Application US/08232513A
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /label= SapC
US-08-232-513A-1
Query Match 58.8%; Score 77; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 0.3;
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXKEXX 27
|:::|:::|:::|:::|:::|
Db 1 CEFVKEVTKLIDNNKTEKIL 22

RESULT 12
US-08-484-594A-1
; Sequence 1, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/484,594A  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/100,247  
;; FILING DATE: 30-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Israel, Ned A  
;; REGISTRATION NUMBER: 29,655  
;; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-235-8550  
;; TELEFAX: 619-235-0176  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
US-08-484-594A-1  
  
Query Match 58.8%; Score 77; DB 1; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.3;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CEXXXKXXXXXNDNNKXKEXX 27  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22  
  
RESULT 13  
US-09-231-159-1  
; Sequence 1, Application US/09231159  
; Patent No. 6268347  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-8949  
; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-09-231-159-1  
  
Query Match 58.8%; Score 77; DB 4; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.3;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CEXXXKXXXXXNDNNKXKEXX 27  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22  
  
RESULT 14  
US-08-611-307-1  
; Sequence 1, Application US/08611307  
; Patent No. 6271196  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611,307  
; FILING DATE: 05-MAR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-611-307-1  
  
Query Match 58.8%; Score 77; DB 4; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.3;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CEXXXKXXXXXNDNNKXKEXX 27  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22  
  
RESULT 15  
US-09-148-030-1  
; Sequence 1, Application US/09148030C  
; Patent No. 6458357  
; GENERAL INFORMATION:  
; APPLICANT: White, Michael T.  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Wright, David E.  
; TITLE OF INVENTION: RETRO-INVERSO NEUROTROPHIC AND ANALGESIC



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; TITLE OF INVENTION:  PEPTIDES
; FILE REFERENCE:  MYELOS.004CPI
; CURRENT APPLICATION NUMBER:  US/09/148,030C
; CURRENT FILING DATE:  1998-09-03
; PRIOR APPLICATION NUMBER:  08/926,015
; PRIOR FILING DATE:  1997-09-09
; NUMBER OF SEQ ID NOS:  12
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH:  22
; TYPE:  PRT
; ORGANISM:  Homo Sapien
US-09-148-030-1

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Query Match 58.8%; Score 77; DB 4; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.3;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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QY      6 CEXXXKEXXXXXNNKXEXX 27
      ||::||::||::||::||::||::
DB      1 CEFVKEVTKLIDNNKTEKIL 22
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Search completed: June 2, 2003, 14:20:42  
Job time : 16 secs







US-10-060-036-73  
; Sequence 73, Application US/10060036



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; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-949-713-10
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Best Local Similarity 23.1%; Pred. No. 1.3e+02;
Matches 9; Conservative 23; Mismatches 6; Indels 1; Gaps 1;

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Db 99 DPCTKCEHGIKECTLTSTNTKCEGSRSEKPKSCDKTH 137
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Search completed: June 2, 2003, 14:21:06  
Job time : 17 secs

